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OM protein - protein search, using sw model  
Run on: March 17, 2003, 08:47:27 ; Search time 35 seconds  
Sequence: 1 MPQAESTPOTLYDKVLQAHV.....KAVPVPTTNRGEBKEPLEW 778  
Scoring table: BL25062  
Gapop 10.0 , Gapext 0.5

Title: US-10-010-227-3  
Perfect score: 4055  
Searched: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : SPTREMBL 21:  
1: sp\_archaea:  
2: sp\_bacteria:  
3: sp\_fungi:  
4: sp\_human:  
5: sp\_invertebrate:  
6: sp\_mammal:  
7: sp\_mhc:  
8: sp\_organelle:  
9: sp\_phage:  
10: sp\_plant:  
11: sp\_rabbit:  
12: sp\_virus:  
13: sp\_vertebrate:  
14: sp\_unclassified:  
15: sp\_virus:  
16: sp\_bacteria:  
17: sp\_archeap:  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query	Match Length	DB ID	Description
1	2431.5	60.0	711	3 Q9BY5	Q9b3Y5 yarrowia li
2	1636.4	40.3	469	16 Q92176	Q92176 rhizobium m
3	1611.3	39.7	469	16 Q8YJC9	Q8YJC9 brucella m
4	1586.5	39.1	475	16 Q8BY9Y	Q8BY9 agrobacteri
5	1567.9	38.7	469	16 Q98EF1	Q98EF1 rhizobium l
6	1563.6	38.5	448	2 Q9EV53	Q9EV53 rhizobium m
7	1562.7	38.5	479	16 Q9ABNO	Q9ABNO caulobacter
8	1549.5	38.2	469	16 Q97Z15	Q97Z15 neisseria m
9	1507.5	37.2	474	16 Q9JU82	Q9JU82 neisseria m
10	1498.0	37.0	474	16 Q9PXY3	Q9PXY3 pseudomonas
11	1493.12	36.8	469	16 Q8XX3	Q8XX3 xylella fas
12	1469.5	36.2	466	16 Q8X400	Q8X400 ralstonia s
13	1469.5	36.2	466	16 Q8Z1H0	Q8Z1H0 escherichia
14	1452.35	35.8	476	16 Q9K81	Q9K81 yersinia pe
15	1425.5	35.8	467	16 Q9K81	Q9K81 vibrio chol
16	1396.34	472	16 Q9K8F0	Q9K8F0 bacillus ha	

17 1385.5 34.2 476 16 Q86534 streptomyce  
18 1354.5 33.4 466 16 Q85072 buchnera ap  
19 1354.5 33.4 469 2 Q85065 buchnera ap  
20 1315.5 32.4 448 2 Q8EVF9 buchnera ap  
21 1311.5 32.3 470 16 Q9PLW1 camyloact  
22 1290.5 31.8 466 031293 buchnera ap  
23 1283.5 31.7 462 16 Q92A26 Q92A26 listeria in  
24 1282.5 31.6 456 16 Q99SJ3 straphylococ  
25 1280.5 31.6 442 2 Q8EVH1 buchnera ap  
26 1279.5 31.6 462 16 Q8Y5R7 listeria mo  
27 1275.5 31.5 443 2 Q8EVIO buchnera ap  
28 1271.5 31.4 444 2 Q8EVG8 buchnera ap  
29 1259.5 31.1 443 2 Q8EVG5 buchnera ap  
30 1253.5 30.9 443 2 Q8EV15 buchnera ap  
31 1252.5 30.9 442 2 Q8EVH buchnera ap  
32 1244.5 30.7 436 2 Q8AJ49 buchnera ap  
33 1240.5 30.6 436 2 Q8AJ73 buchnera ap  
34 1238.5 30.5 436 2 Q8AJ47 buchnera ap  
35 1238.5 30.5 443 2 Q8EVH4 buchnera ap  
36 1236.5 30.5 443 2 Q8EVG2 buchnera ap  
37 1230.5 30.3 436 2 Q8AJ52 buchnera ap  
38 1227.5 30.3 442 2 Q8EVH7 buchnera ap  
39 1225.5 30.2 444 2 Q8EVIO buchnera ap  
40 1222.5 30.1 433 2 Q89Q99 buchnera ap  
41 1217.5 30.0 473 16 Q8ZRJ0 Q8ZRJ0 salmonella  
42 1211.5 29.9 492 2 Q8EVG3 buchnera ap  
43 1209.5 29.8 472 2 Q92ND5 buchnera ap  
44 1194.5 29.5 456 2 Q94IM3 buchnera ap  
45 1172.5 28.9 467 16 Q8YX02 anaerobacteria  
46 1170.5 28.9 418 2 Q9AJ50 buchnera ap  
47 1055.5 26.3 369 2 Q9AQ66 buchnera ap  
48 699.5 17.3 418 17 Q8TVEF2 methanopyru  
49 660.5 16.3 424 17 Q8TFL1 methanobarc  
50 656.5 16.2 424 16 Q8U2A1 methanococcus  
51 641.5 15.8 431 16 Q8RTI6 methanococcus  
52 640.5 15.8 659 16 Q9W565 aquifex aeo  
53 637.5 15.7 423 17 Q8U207 pyrococcus  
54 637.5 15.5 415 16 Q8VMA6 methanopyru  
55 612.5 15.1 641 16 Q8RCFB methanobarc  
56 599.5 14.8 642 16 Q87KE8 methanococcus  
57 597.5 14.7 211 17 Q8YCW7 methanococcus  
58 595.5 14.7 417 16 Q8W224 thermotoga  
59 588.5 14.5 201 16 Q88E51 methanococcus  
60 576.5 14.2 422 16 Q8TEEO methanococcus  
61 570.5 14.1 509 10 Q84AR8 methanococcus  
62 562 13.9 420 17 Q8TQZ3 methanococcus  
63 562 13.9 661 17 Q8HMF1 halobacteri  
64 560.5 13.8 216 16 Q8UBR0 halobacteri  
65 558.5 13.8 509 10 Q8P014 halobacteri  
66 555.5 13.7 552 13.6 721 3 Q9UT74 halobacteri  
67 552 13.6 544 13.4 213 16 Q8QUB1 halobacteri  
68 542 13.4 69 69 16 Q8HZ4 halobacteri  
69 542 13.4 213 16 Q8JZ16 halobacteri  
70 541.5 13.4 71 71 16 Q8WY77 halobacteri  
71 541.5 13.2 72 72 16 Q86VU1 halobacteri  
72 536.5 13.2 73 73 16 Q8XXX4 halobacteri  
73 535 13.2 216 16 Q8XXX4 halobacteri  
74 533 13.1 201 2 Q8R998 halobacteri  
75 523.5 12.9 418 16 Q8R998 halobacteri  
76 519 12.8 215 16 Q8PAK1 halobacteri  
77 513 12.7 202 16 Q8ABNI halobacteri  
78 512 12.6 434 16 Q8TY9 halobacteri  
79 511.5 12.6 418 16 Q8BDK2 halobacteri  
80 506 12.5 201 16 Q8Z913 halobacteri  
81 500.5 12.3 201 16 Q8CJN8 halobacteri  
82 498 12.3 200 16 Q8R80 halobacteri  
83 492 12.1 201 16 Q8X401 halobacteri  
84 482 11.9 768 4 Q9UQZ1 halobacteri  
85 474.5 11.7 780 4 Q8TQ06 halobacteri  
86 474 11.7 200 16 Q8Z1H1 halobacteri  
87 473.5 11.7 780 11 Q8Z1K0 halobacteri  
88 472.5 11.7 780 11 Q8R34 halobacteri  
89 472.5 11.7 787 11 Q8NFX1 halobacteri

90	470.5	11.6	778	3	074699	aspergillus	Qy	189	GVSSKVYVLLHAIGIICPAGGTGAVIEFOGSVIRSLNSARMSTMNSIEGGARAGMVAPD	248	
91	467	11.5	194	16	Q9K8F1	baillius ha	Db	182	GITSKDLILHITGIVTGTAGGTCTVIEFCGEAIRDLSMEARMSCNMALEGGARAGMIAPD	241	
92	463	11.4	905	3	Q9P7D4	schizosacch	Qy	249	ETTEPEYIKGRPLAPKDSPEWHKATQYWKNLSDPGAKYDIDVFDIAKDIVPTLTWGTS	308	
93	457	11.3	809	3	Q9HEA5	neurospora	Db	242	ETTEFVTRGRPLAP-EGAAENEKAFTWWTLHSDSDAEFDIDYNIKGEDIIPIVWGTS	299	
94	455	11.2	788	5	Q9NGC3	daphnia pul	Qy	309	EDVWPTPTGVPPDPETIATEKAADGRMLQTMGLKAGRPMPEDPVDKVFIGSCTNSR	368	
95	447	11.0	415	17	Q8R2W41	pyrobaculum	Db	300	QDALTPTGSVDPDKSKESDPIRAGIBALETMGLEANTPLNEAVDKVFIGSCTNSR	359	
96	442	10.9	747	2	Q8Rp87	bacteroides	Qy	369	LRAAAAVVKGRKRAPNYSKAMVPGSSVLUVKTQAEEGSLDKIFEEAGFWR	428	
97	442	10.9	683	5	Q9VTE8	Q9vies droophil	Db	360	LRAAAAVVRGKEDSVVRAMVPGSSVLUVKRTEAEAGLDKVPEAAGFWR	419	
98	441	10.9	402	17	Q8Tw9	methanophorus	Qy	429	NPDILAQERCASTSNENPFGQAGGERTHLMSPVMAAAGIVGKLA	480	
99	440	10.9	415	17	Q974R0	sulfolobus	Db	420	NPDILNPRERCASTSNENPFGQALSRTHLVSPAMAALAGITGKLTDVRYLPKDEAKI	479	
100	438	10.8	196	2	Q9AIM2	streptococc	Qy	481	T-----DYSRASPTHAAYQSYTKEH-VDTRINQDAHEKIDATIDPENNNGPH	527	
<b>ALIGNMENTS</b>											
<b>RESULT 1</b>											
Q9P7Y5			PRELIMINARY;		PRT;	711 AA.	Db	480	VIGEDDEMAEKYDEKEQPAVKKMKPATVQDQVDEQDVAE-----	524	
ID	Q9P3Y5;			DT	01-OCT-2000	(TREMBLrel. 15, Created)	Db	528	TNTSASVGTSAQGLPKETILKGTAAPLEKANYDTDALIPKOFKLTIKRTGLGNALFYEMRF	587	
AC	Q9P3Y5;			DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)	Db	525	-NITS-----	580	
				DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)	Db	588	NE-DG-TEKSDFVNLKEPYRKASILYCTGANPGCSSREHAPWALDGFIRSYIAPSAD	645	
GN	LB01.			DE	3-isopropylmalate dehydratase (EC 4.2.1.33) (Fragment).		Db	581	KEVDGQEKQTDFMLVAPWDXASILVSGNNFGCSSREHAPWALAEGIRCIAAPSFGD	640	
LNBU1.				OS	Yarrowia lipolytica (Candida lipolytica).		Qy	646	IFFNNFSKPNGLPILPKDQAEQIAEAAAGREKETTCFEEBF	705	
				OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;		Db	641	IYNNFSKPNGLPILPVADVIKSKLMPVADKGSILTVDPNQKVLLGDEVLFVEVEDF	700	
				OX	Saccharomycetales; Dipodascaceae; Yarrowia.		Qy	706	RKHCLVNGLDD	716	
				RN	[1] — TaxID=4952;		Db	701	RKHCRVNGLDD	711	
				RP	SEQUENCE FROM N.A.		RESULT 2				
				RC	STRAIN=2122;		Q92L76		PRELIMINARY;	PRT;	469 AA.
				RC	PubMed:11489863;		AC	Q92L76;			
				RA	RAuerberger S., Wang H., Gaillardin C., Barth G., Nicaud J.M.;		DT	Q92L76;			
				RA	Insertional mutagenesis in the n-alkane-assimilating Yeast Yarrowia		RA	Q92L76;			
				RA	lipolytica: Generation of tagged mutations in genes involved in		RA	Q92L76;			
				RA	hydrophobic substrate utilization.";		RA	Q92L76;			
				RA	J. Bacteriol. 183:5102-5109 (2001).		RA	Q92L76;			
				RA	EMBL; Aa278653; CAB94451; --.		RA	Q92L76;			
				RA	InterPro; IPK00573; Aconitase_C.		RA	Q92L76;			
				RA	InterPro; IPK001030; Aconitase_N.		RA	Q92L76;			
				RA	InterPro; IPK001899; Gram_pos_anchor.		RA	Q92L76;			
				RA	InterPro; IPK004431; LeuD.		RA	Q92L76;			
				RA	Pfam; PF003330; aconitase_1.		RA	Q92L76;			
				RA	Pfam; PF006949; Aconitase_C_1.		RA	Q92L76;			
				RA	PRINTS; PRO0015; ACONITASE.		RA	Q92L76;			
				RA	ProDom; PD000511; Aconitase_N; 1.		RA	Q92L76;			
				RA	TIGRFams; TIGR00170; leuc_1.		RA	Q92L76;			
				RA	TIGR00171; leuD_1.		RA	Q92L76;			
				RA	PROSITE; PS00450; ACONITASE_1; 1.		RA	Q92L76;			
				RA	PROSITE; PS01244; ACONITASE_2; 1.		RA	Q92L76;			
				RA	PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.		RA	Q92L76;			
				KW	KW Lyase.		RA	Q92L76;			
				FT	NON_TER 711 AA;	711	RA	Q92L76;			
				FT	SEQUENCE 711 AA;	77476 MW;	RA	Q92L76;			
				FT	996407A7F7B1AF2E CRC64;		RA	Q92L76;			
				FT	Query Match 60.0% Score 242.5; DB 3; Length 711;		RA	Q92L76;			
				FT	Best Local Similarity 65.7%; Pred. No. 1e-15; Indels 45; Gaps 9;		RA	Q92L76;			
				FT	Matches 480; Conservative 76; Mismatches 130; Gaps 45; Gaps 9;		RA	Q92L76;			
				FT	9 QTYLDKVQLQAHVYDEKLDTGTVLILYIDRHLVHEVTSQAFEGLRNAGRAKVRPDCTLATTD 68		RA	Q92L76;			
				FT	3 QTYLDKVQLQAHVYDEKLDTGTVLILYIDRHLVHEVTSQAFEGLRNAGRAKVRPDCTLATTD 61		RA	Q92L76;			
				FT	62 HNIPITTRKDFKSIGTKEEDSRQLQTCVLEENYKEFGTYVFGSLDKRQGIVYHVGPEQ 128		RA	Q92L76;			
				FT	69 HNVPITTSRKALDIAFKEEDSRQLQTCVLEENYKEFGTYVFGSLDKRQGIVYHVGPEQ 128		RA	Q92L76;			
				FT	129 FFLPGTIVVCGDSHTSSTHGAFLAFLGIGTSEVHVLATQCLIKTSKMRTOVGDGLAP 188		RA	Q92L76;			
				FT	122 FFLPGTIVVCGDSHTSSTHGAFLAFLGIGTSEVHVLATQCLIKTSKMRINVSGKLQP 181		RA	Q92L76;			
				FT	Query Match 60.0% Score 242.5; DB 3; Length 711;		RA	Q92L76;			
				FT	Best Local Similarity 65.7%; Pred. No. 1e-15; Indels 45; Gaps 9;		RA	Q92L76;			
				FT	Matches 480; Conservative 76; Mismatches 130; Gaps 45; Gaps 9;		RA	Q92L76;			
				FT	9 QTYLDKVQLQAHVYDEKLDTGTVLILYIDRHLVHEVTSQAFEGLRNAGRAKVRPDCTLATTD 68		RA	Q92L76;			
				FT	3 QTYLDKVQLQAHVYDEKLDTGTVLILYIDRHLVHEVTSQAFEGLRNAGRAKVRPDCTLATTD 61		RA	Q92L76;			
				FT	62 HNIPITTRKDFKSIGTKEEDSRQLQTCVLEENYKEFGTYVFGSLDKRQGIVYHVGPEQ 128		RA	Q92L76;			
				FT	69 HNVPITTSRKALDIAFKEEDSRQLQTCVLEENYKEFGTYVFGSLDKRQGIVYHVGPEQ 128		RA	Q92L76;			
				FT	129 FFLPGTIVVCGDSHTSSTHGAFLAFLGIGTSEVHVLATQCLIKTSKMRTOVGDGLAP 188		RA	Q92L76;			
				FT	122 FFLPGTIVVCGDSHTSSTHGAFLAFLGIGTSEVHVLATQCLIKTSKMRINVSGKLQP 181		RA	Q92L76;			

DR	TIGRFAMS;	TIGR00170;	leuC;	1.
DR	PROSITE;	PS0050;	ACONITASE_1;	1.
DR	PROSITE;	PS01244;	ACONITASE_2;	UNKNOWN_1.
KW	Lyase;	Complete protease.		
SQ	SEQUENCE	469 AA;	50994 MW;	22A2F7D040645726 CRC64;
Query	Match	40.3%	Score 1636;	DB 16; Length 469;
Best Local Similarity	66.0%	Pred. No. 3	3e-102;	
Matches	313;	Conservative	57;	Mismatches 96;
				Indels 8; Gaps 3;
QY	6 STPQTYLKVQAHVYDEKLDTGTVLYIDRHLVHEVTSPOAFEGLNAGRKVRPDTLA	65		
Db	2 SAPRTLYDKIMDHVYDQEDGTCILLYIDRHLVHEVTSPOAFEGLNAGRKVRPDTLA	61		
QY	126 EQGFTLPGTTVCGDSHTSTGAGFAGLAAGFTGTCSEVHVLATQCLTRSKNMRLQDGE	185		
Db	117 EQGFTLPGMTIVCGDSHTSTGAGFAGLAAGFTGTCSEVHVLATQCLTRSKNMRLQDGE	176		
QY	186 LARGVSSKDVLHAIGITGAGGTGAVIEFGSVIISLMSARMSCNMSTEGGARAGMV	245		
Db	177 LPGVYAKDVLHAIGITGAGGTGAVIEFGSVIISLMSARMSCNMSTEGGARAGLV	236		
QY	246 APDEITFEYLKGRPLAKYDSEPHWKTQYWKNUQLOSPGAKVDDIDPDAKDIVPILWG	305		
Db	237 APDEITFEYIKRKPRAKPEA-WDRAWEYKMLHDEGAHYDRVWVLDAAMLPPIVSWG	294		
QY	306 TSPEDVWVPIGTVGVPDPETFATEAKKADGRMRMQLYQMGKLAGTPEMDIDPVDRPIGSCNRS	365		
Db	295 SSPEPDVSVIGVVPNPEDDIQDETAKRASKWRLADYMGKPGKTTIDAVDRPIGSCNRS	354		
QY	366 IEDLRAAAWVKGKRPKPNVKSAMVPGSGLQKTOQEEBEGLQKIFERAGFPEWREAGCSMC	425		
Db	355 IEDLRAAAWVKGKRPKVTW-SAMIVPGSGLQKQEQAEGLQKIFERAGFPEWREAGCSMC	413		
QY	426 LGMNPDLAPOBRCASTSNRNFEGRQGAGGRTHLMSVMAAAGIVKLADVR	479		
Db	414 LAMNDRDKLPGERCASTSNRNFEGRQGFKRTHLSPAMAAAAGAVGHFVDIR	467		
RESULT	3			
Q8YJC9	ID	Q8YJC9	PRELIMINARY;	PRY;
AC	OBYJC9;			469 AA.
DT	01-MAR-2002 (TREMBLrel. 20, Created)			
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)			
DE	3-isopropylmalate dehydratase large subunit (EC 4.2.1.33).			
GN	BME0157.			
OS	Bacillus			
OC	Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;			
OC	Brucellaceae; Brucella.			
OX	NCBI_TaxID=29459;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	STRAIN=46M / ATCC 34456 / BIOTYPE 1;			
RX	MEDLINE=20020109; PubMed=11756688;			
RA	DelVecchio V.G., Kapitar V., Redkar R.J., Patra G., Mujer C., Los T.,			
RA	Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,			
RA	Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Gotsman E.,			
RA	Seklov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,			
RA	Haselkorn R., Kyrides N., Overbeek R.;			
RT	"The genome sequence of the facultative intracellular pathogen			
RT	Brucella melitensis.;"			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).			
DR	EMBL; AE009459; AAL51391; -.			
DR	InterPro; IPR001030; Aconitase_N.			
DR	InterPro; IPR004430; LeuC.			
DR	PFAM; PF00330; aconitase_1.			
DR	PRINTS; PR00015; ACONITASE.			
DR	ProDom; PD000511; Aconitase_N; 1.			
DR	TIIGRFAMS;	TIGR00170;	leuC;	1.
DR	PROSITE;	PS0050;	ACONITASE_1;	1.
DR	PROSITE;	PS01244;	ACONITASE_2;	UNKNOWN_1.
KW	Lyase;	Complete protease.		
SQ	SEQUENCE	469 AA;	5092 MW;	14442D94C40BCDF CRC64;
Query	Match	39.7%	Score 1611;	DB 16; Length 469;
Best Local Similarity	66.8%	Pred. No. 1	6e-100;	
Matches	316;	Conservative	51;	Mismatches 98;
				Indels 8; Gaps 3;
QY	6 STPQTYLKVQAHVYDEKLDTGTVLYIDRHLVHEVTSPOAFEGLNAGRKVRPDTLA	65		
Db	2 SAPRTLYDKIMDHVYDQEDGTCILLYIDRHLVHEVTSPOAFEGLNAGRKVRPDTLA	61		
QY	126 EQGFTLPGTTVCGDSHTSTGAGFAGLAAGFTGTCSEVHVLATQCLTRSKNMRLQDGE	185		
Db	117 EQGFTLPGMTIVCGDSHTSTGAGFAGLAAGFTGTCSEVHVLATQCLTRSKNMRLQDGE	176		
QY	186 LARGVSSKDVLHAIGITGAGGTGAVIEFGSVIISLMSARMSCNMSTEGGARAGMV	245		
Db	177 LPGVYAKDVLHAIGITGAGGTGAVIEFGSVIISLMSARMSCNMSTEGGARAGLV	236		
QY	246 APDEITFEYLKGRPLAKYDSEPHWKTQYWKNUQLOSPGAKVDDIDPDAKDIVPILWG	305		
Db	237 APDEITFEYIKRKPRAKPEA-WDRAWEYKMLHDEGAHYDRVWVLDAAMLPPIVSWG	294		
QY	306 TSPEDVWVPIGTVGVPDPETFATEAKKADGRMRMQLYQMGKLAGTPEMDIDPVDRPIGSCNRS	365		
Db	295 SSPEPDVSVIGVVPNPEDDIQDETAKRASKWRLADYMGKPGKTTIDAVDRPIGSCNRS	354		
QY	366 IEDLRAAAWVKGKRPKPNVKSAMVPGSGLQKTOQEEBEGLQKIFERAGFPEWREAGCSMC	425		
Db	355 IEDLRAAAWVKGKRPKVTW-SAMIVPGSGLQKQEQAEGLQKIFERAGFPEWREAGCSMC	413		
QY	426 LGMNPDLAPOBRCASTSNRNFEGRQGAGGRTHLMSVMAAAGIVKLADVR	479		
Db	414 LAMNDRDKLPGERCASTSNRNFEGRQGFKRTHLSPAMAAAAGAVGHFVDIR	467		
RESULT	4			
Q8YJC9	ID	Q8YJC9	PRELIMINARY;	PRY;
AC	OBYJC9;			475 AA.
DT	01-JUN-2002 (TREMBLrel. 21, Created)			
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)			
DE	3-isopropylmalate dehydratase large subunit (EC 4.2.1.33).			
GN	BME0157.			
OS	Bacillus			
OC	Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;			
OC	Brucellaceae; Brucella.			
OX	NCBI_TaxID=176299;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21608550; PubMed=11743193;			
RA	Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.-P., Woo L.,			
RA	Okura V.K., Zhou Y., Chen L., Wood G.B., Almeida N.F. Jr., Woo L.,			
RA	Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovée D. Sr., Chapman P., Clendening J., Deatherage G., Gillett W., Grant C.,			
RA	Kutayavin T., Levy R., Li M.-J., McClellan E., Palmeri A., Romero P., Gordon D.,			
RA	Raymond C., Rouse G., Saenphimmachak C., Wu Z., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,			
RA	Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,			
RA	Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Nester E.W.,			
RA	"The genome of the natural genetic engineer Agrobacterium tumefaciens C5B;"			
RT	Science 294:2317-2323 (2001).			
RL	[2]			



DR	EMBL; AJ296268; CAC14578_1; -.	RA	Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
DR	InterPro; IPR001030; Aconitase_N.	RT	"Complete genome sequence of <i>Caulobacter crescentus</i> ."
DR	InterPro; IPR004430; LeuC.	RL	Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR	Pfam; PF00330; aconitase; 1.	DR	EMBL; AE005694; AAC22183_1; -.
DR	PRINTS; PR00415; ACONITASE.	DR	TIGR; CC0196; -.
DR	PRODOM; PD000511; Aconitase_N; 1.	DR	InterPro; IPR001030; Aconitase_N.
DR	TIGRFAMS; TIGR00170; leuC; 1.	DR	InterPro; IPR004430; LeuC.
DR	PROSITE; PS00450; ACONITASE_1; 1.	DR	Pfam; PF00330; aconitase; 1.
DR	PROSITE; PS01244; ACONITASE_2; UNKNOWN_1.	DR	PRINTS; PR00415; ACONITASE.
KW	Isomerase.	DR	PRODOM; PD000511; Aconitase_N; 1.
FT	NON_TER 1	DR	TIGRFAMS; TIGR00170; leuC; 1.
SO	SEQUENCE 448 AA; 48466 MW; 029B65EA51A054BD CRC64;	DR	PROSITE; PS00450; ACONITASE_1; 1.
Query Match	38.5%; Score 1563; DB 2; Length 448;	DR	PROSITE; PS01244; ACONITASE_2; UNKNOWN_1.
Best Local Similarity	66.1%; Pred. No. 2. 6e-97;	KW	Complete proteome.
Matches	300; Conservative 53; Mismatches 93; Indels 8; Gaps 3;	SQ	DR
QY	26 DGTGVLYIYDRILVHEVTPSQAPEGLRNAGRKVRVRPDTLATDHNVPTTSRKALKDQIASP 85	DR	KW
Db	1 DGTCLLYIDVCLHLVHEVTPSQAPEGLRNAGRKVRVRPDTLATDHNVPTTSRKALKDQIASP 85	DR	Complete proteome.
QY	86 IKEDDSRTQCVTLEENENKEFVYFGSLSKDKQGIVVINGPQGFTPTGTTVCGDSHTST 145	DR	SQ
Db	56 IKNEEBRIQVEALARNAKADLGVEYYSENDKROGIVHVGPEGFTLPGMTLVCGDHTST 115	DR	Best Local Similarity 38.5%; Score 1562; DB 16; Length 479;
QY	146 HGAFGALALGICGTSEVERVLAQOCITRKSKNRIQVGDGELAPGVSKDVHLAIGIGT 205	DR	Matches 307; Conservative 53; Mismatches 105; Indels 12; Gaps 5;
Db	116 HGAFGALALGICGTSEVERVLAQOCITRKSKNRIQVGDGELAPGVSKDVHLAIGIGT 175	DR	QY 9 QTYLDKULQAHVDEKUDGTWLYIDRHLVHEVTSQAPEGLRNAGRKVRVRPDTLATD 68
QY	206 AGGTGAVIEFCOSVIRSLSMEARMSICMSICMSLEGGARAGMVADEDETFYLKCRPLAKYD 265	DR	Db 4 KLYDKWIDAHVSE-AGGEAATLYDQBLHLHBTQFAFASRAADRKRVRPDRTLAVAD 62
Db	176 AGGTGAVIEFCOSVIRSLSMEARMSICMSICMSLEGGARAGMVADEDETFYLKCRPLAKYD 235	DR	QY 69 RNVPTSRKALKDQIASPIKEDDSRTQCVTLEENENKEFVYFGSLSKDKQGIVHVGPEQ 128
QY	266 SPEWHKATQYWNKLQSDPAGKIDIVDIDVAKDQVITQVDPDDETA 325	DR	Db 63 HNIPTECGALGVD--VADBEARQLQKTLARNVADNGIEFPMSGIRNGVTVHVGPEQ 119
Db	236 A--WDRAYEWKYLHMDGEGAHYDRVVVDAANLPPVPSVWGSSEDVPSVQGVVPNPDQ 293	DR	QY 129 FTLPGTTWVGDSHTSTHGARGALALGICGTSEVERVLAQOCITRKSKNRIQVGDGLAP 188
QY	326 TEAKKADGRRMLQYMGMLKAGTPMEDIPDVKVGICSTNSRTEDLRAAAAVWKGKAPPV 385	DR	Db 120 RTQPGMTVCGDSHTSTHGARGALALGICGTSEVERVLAQOCITRKSKNRIQVGDGLAP 179
Db	294 DETKRTSKWRLDYMGLPKPTKTDIAIDRVFGSCTNGRIBLRAVEVWGRKVSPV 353	DR	QY 189 GVSXKDVHLAIGIGTAGGAGVIERPGSVIRSLSMEARMSICMSICMSLEGGARAGMVADEDETFYLKCRPLAKYD 248
QY	386 KSAMVWVGSGLVKTYQABEGLDKIFEEAGPENREAGGSMCLGNPNDLQAPQCASTNSR 445	DR	Db 180 GVTGDKVALAVIGEIGTAGGAGVIEPAGEATAGLSMEGRMTLICNTLIEGGAKAGLVAD 239
Db	354 -SAMVWVGSGLVKTYQABEGLDKIFEEAGPENREAGGSMCLGNPNDLQAPQCASTNSR 412	DR	QY 249 ETEFVYKGPKLAKYDPSPEWKATQWNLQSDPGKQYDIDVFDKQDIPVITLITGSP 308
QY	446 NFGRCGAGGRTHLSPVMAAGIYGKGLADRK 479	DR	Db 240 DKTFFAYVQGKPAK--GAQWMLSHWKTFTDEAVFDRTVWIGSALVEMVNTGTP 297
Db	413 NFGRCGAGGRTHLSPVMAAGIYGKGLADRK 446	DR	QY 309 EDVPPITGCVVPPRETEAKKQDGRLQMLQYMGMLKAGTPMEDIPDVKVGICSTNSRTE 368
RESULT 7		DR	Db 298 EDVPPITGCVVPPRETEAKKQDGRLQMLQYMGMLKAGTPMEDIPDVKVGICSTNSRTE 357
Q9ABNO	OPABNO PRELIMINARY; PRT; 479 AA.	DR	QY 369 LRAAAVTK---GRKPKAPTKSAMVPGSGLVKTQAEBGLKIFEEAGGEWREAGCS 423
ID	OPABNO; AC	DR	Db 358 MRAAAAVWQEAFLHGRLVAPYHK-AMVPGSGLVKEQABEGLDIAFKAGFDWREPGCS 416
DT	01-JUN-2001 (TREMBlre. 17, Last sequence update)	DR	QY 424 MCGMNPDLQAPQCASTNSRNFEGRCGAGGRTHLSPVMAAGIYGKGLADRK 480
DT	01-JUN-2001 (TREMBlre. 17, Last sequence update)	DR	Db 417 MCLAMNPDLQAPQCASTNSRNFEGRCGAGGRTHLSPVMAAGIYGKGLADRK 473
DE	3-isopropylmalate dehydratase, large subunit.	DR	Q9Z215
GN	C00196.	DR	Q9Z215 PRELIMINARY; PRT; 469 AA.
OS	OSCAulobacter crescentus.	AC	Q9Z215;
OC	Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;	DT	01-OCT-2000 (TREMBlre. 15, Last sequence update)
OC	NCBI_TaxID=155892;	DT	01-OCT-2000 (TREMBlre. 15, Last sequence update)
RN	[1]	DT	01-OCT-2000 (TREMBlre. 21, Last annotation update)
RP	SEQUENCE FROM N-A.	DT	01-JUN-2002 (TREMBlre. 21, Last annotation update)
RC	STRAIN=ATCC 19089 / CB15;	DE	3-isopropylmalate dehydratase, large subunit.
RX	MEDLINE:21173698; PubMed=11259647;	GN	GNM036.
RA	Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Eisen J.J., Heidelberg J.F., Ailey M.R.K., Oita N., Maddock J.R., RA	OS	Neisseria meningitidis (serogroup B).
RA	Poocka I., Nelson W.C., Newton C., Phakee N.D., Bly B., Deoy R.T., Dodson A.S., Gwinn M.L., Haft D.H., RA	OC	Bacterii; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
RA	Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., RA	OX	NCBI_TaxID=491;
RA	Utterback T., Tran K., Wolf A., Vamathevan J., Rimolaeva M., White O., RA	RN	SEQUENCE FROM N-A.
RA	NCBI_TaxID=155892;	RP	SEQUENCE FROM N-A.
RA	MEDLINE:21173698; PubMed=11259647;	RC	STRAIN=MCS8 / SEROCROU B;
RA	MEDLINE:201755; PubMed=10710307;	RX	RA
RA	Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Pedersen J.F., Dodson R.J., RA	RA	Eisen J.A., Ketchum K.A., Hood D.W., Pedersen J.F., Hickey E.K., Nelson W.C., Gwinn M.L., Deoy R.T., Petersen J.D., Hickey E.K., RA
RA	Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., RA	RA	Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., RA

RESULT 9									
Query	Match	Score	Length	Start	End	Sequence	Start	End	Sequence
Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vanathavan J., Gill J., Scariato V., Masiagnani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rapuoli R., Venter J.C., "Complete genome sequence of <i>Neisseria meningitidis</i> serogroup B strain MC58.", Science 287:1809-1815 (2000).	Q9JU82; EMBL; AE002454; AAF141351; -.	38.2%	469	PF00320; PR0415; ACONITASE.	PF00320; PR0415; ACONITASE.	PF00320; PR0415; ACONITASE.	PR0415; ACONITASE.	PR0415; ACONITASE.	PR0415; ACONITASE.
TIGR; NMB136; InterPro; IPR001030; Aconitase_N.	TIGR; NMB136; InterPro; IPR001030; Aconitase_N.	63.6%	9	Pred. No.	Mismatches	Length 469; DB 16; Index 102; Indels 9; Gaps	2.6e-96;	1	1
PR0415; ACONITASE.	PR0415; ACONITASE.	63.6%	9	1	1	1	1	1	1
TIGRFAMS; TIGR00170; leuc.; 1.	TIGRFAMS; TIGR00170; leuc.; 1.	63.6%	9	1	1	1	1	1	1
PS000450; ACONITASE_1.	PS000450; ACONITASE_1.	63.6%	9	1	1	1	1	1	1
PS01244; ACONITASE_2.	PS01244; ACONITASE_2.	63.6%	9	1	1	1	1	1	1
Complete protein.	Complete protein.	63.6%	9	1	1	1	1	1	1
SEQUENCE 469 AA;	SEQUENCE 469 AA;	63.6%	9	1	1	1	1	1	1
50843 MW;	50843 MW;	63.6%	9	1	1	1	1	1	1
D536C334590E400 CRC64;	D536C334590E400 CRC64;	63.6%	9	1	1	1	1	1	1
Best Local Similarity	Query Match	Score	Length	Start	End	Sequence	Start	End	Sequence
Matches 302;	Best Local Similarity	38.2%	469	7	7	T P Q T L D K V L Q A H Y D E K L D G T V L Y I D R H L V H E Y T S P O A F E G L R N A G R K V Y R P D C T L A T	125	166	T P Q T L D K V L Q A H Y D E K L D G T V L Y I D R H L V H E Y T S P O A F E G L R N A G R K V Y R P D C T L A T
Conservative	Best Local Similarity	63.6%	469	2	2	T A Q I L D K L W N S H V R E E D G T V L Y I D R H L V H E Y T S P O A F E G L R N A G R K V Y R P D C T L A T	166	207	T A Q I L D K L W N S H V R E E D G T V L Y I D R H L V H E Y T S P O A F E G L R N A G R K V Y R P D C T L A T
Mismatches	Best Local Similarity	63.6%	469	67	67	T D H N V P T S R K A L K D I A S F T K E D D S R T C V T L E R N K E F G - V T Y R G L S D K R Q G I T Y V I G P	125	246	T D H N V P T S R K A L K D I A S F T K E D D S R T C V T L E R N K E F G - V T Y R G L S D K R Q G I T Y V I G P
Indels	Best Local Similarity	63.6%	469	62	62	A D H I N T P T - - - - - G D W D K G I Q D P I S K L Q V D T D K N I K E F G A L A V T P F M D K Q G Q I T Y V M G P	115	246	A D H I N T P T - - - - - G D W D K G I Q D P I S K L Q V D T D K N I K E F G A L A V T P F M D K Q G Q I T Y V M G P
Gaps	Best Local Similarity	63.6%	469	126	126	E Q G P T L P G T V V C Q D S H T S T H G A R G A L A R G I T S E V E R H A T O C L I T K R S E R N M R I Q D V G E	185	246	E Q G P T L P G T V V C Q D S H T S T H G A R G A L A R G I T S E V E R H A T O C L I T K R S E R N M R I Q D V G E
1	1	1	1	1	1	E Q G A T L P G M T V V C G D S H T S T H G A R G A L A R G I T S E V E R H A T O C L I T K R S E R N M R I Q D V G E	185	246	E Q G A T L P G M T V V C G D S H T S T H G A R G A L A R G I T S E V E R H A T O C L I T K R S E R N M R I Q D V G E
116	116	116	116	116	116	E Q G A T L P G M T V V C G D S H T S T H G A R G A L A R G I T S E V E R H A T O C L I T K R S E R N M R I Q D V G E	185	246	E Q G A T L P G M T V V C G D S H T S T H G A R G A L A R G I T S E V E R H A T O C L I T K R S E R N M R I Q D V G E
186	186	186	186	186	186	L A P G V S K D V V L H A I G I T T A G G T G A V I T E F C G S V I R S L S M E A R M S C I M N S I E G G A R A G M V	245	246	L A P G V S K D V V L H A I G I T T A G G T G A V I T E F C G S V I R S L S M E A R M S C I M N S I E G G A R A G M V
176	176	176	176	176	176	L K A G V T A K D V A L T I I G Q I T A G G T G Y A I T B G G E A I R S L S M E S R U T L C N N A I E A G A R S G M V	235	246	L K A G V T A K D V A L T I I G Q I T A G G T G Y A I T B G G E A I R S L S M E S R U T L C N N A I E A G A R S G M V
235	235	235	235	246	246	A P D E I T F B Y L K G R P L A K P Y D S P E H T K A T Q Y W K N I Q S D P G A K Y D I D F V I D A K D I V T P L T W G	305	246	A P D E I T F B Y L K G R P L A K P Y D S P E H T K A T Q Y W K N I Q S D P G A K Y D I D F V I D A K D I V T P L T W G
236	236	236	236	236	236	A V D Q T T I D Y V K D K P F A P E G E A - - W D K A V E X W R T L V S D E G A V F D K E Y R F N A E D I E F Q V T N G	293	246	A V D Q T T I D Y V K D K P F A P E G E A - - W D K A V E X W R T L V S D E G A V F D K E Y R F N A E D I E F Q V T N G
306	306	306	306	306	306	T S P B D V V P I T G V V P D P E T P A T E A K K A D G E R M L Q Y M G L K A G T P M B D I P V D K V F I G S C T N S R	365	306	T S P B D V V P I T G V V P D P E T P A T E A K K A D G E R M L Q Y M G L K A G T P M B D I P V D K V F I G S C T N S R
294	294	294	294	294	294	T S P B M V D L I S S K Y V P N P A E T D P V Y K R S G M E R A L E M G L E A T P L A N B I P V D F I V F S C T N S R	353	294	T S P B M V D L I S S K Y V P N P A E T D P V Y K R S G M E R A L E M G L E A T P L A N B I P V D F I V F S C T N S R
366	366	366	366	366	366	I E D I R A A A A A V V G S R K K A P V K S A M V P V G S G L V K T Q A E E R G L D K I F E A G F E W R E A G G C S M C	425	366	I E D I R A A A A A V V G S R K K A P V K S A M V P V G S G L V K T Q A E E R G L D K I F E A G F E W R E A G G C S M C
354	354	354	354	354	354	I E D L R E A A A I A D K R K K A A N V R Q V L I V P G S G L V K E Q A E K G L D K I F E A G F E W R E P G C S M C	413	354	I E D L R E A A A I A D K R K K A A N V R Q V L I V P G S G L V K E Q A E K G L D K I F E A G F E W R E P G C S M C
426	426	426	426	426	426	L G M N P D I L A P Q E R C A S T S N R N F E G R Q A G G R T H I M S P M A A A G I V G K L A D V R K L	480	426	L G M N P D I L A P Q E R C A S T S N R N F E G R Q A G G R T H I M S P M A A A G I V G K L A D V R K L
414	414	414	414	414	414	L A M N A D R U L T P G Q R C A S T S N R N F E G R Q A G G R T H I M S P M A A A A A V V G R F D I R M	468	414	L A M N A D R U L T P G Q R C A S T S N R N F E G R Q A G G R T H I M S P M A A A A A V V G R F D I R M
Q9JU82; PRELIMINARY; PRT;	Q9JU82; PRELIMINARY; PRT;	469	AA.	Q9JU82; PRELIMINARY; PRT;	Q9JU82; PRELIMINARY; PRT;	469	AA.	Q9JU82; PRELIMINARY; PRT;	Q9JU82; PRELIMINARY; PRT;
01-OCT-2000 (TREMBL) 1. 15, Created)	01-OCT-2000 (TREMBL) 1. 15, Last sequence update)			01-OCT-2000 (TREMBL) 1. 15, Last sequence update)	01-OCT-2000 (TREMBL) 1. 21, Last annotation update)			01-OCT-2000 (TREMBL) 1. 21, Last annotation update)	01-OCT-2000 (TREMBL) 1. 21, Last annotation update)
(REC 4.2.1.33)	Putative 3-isopropylmalate dehydratase large subunit			(REC 4.2.1.33)	Putative 3-isopropylmalate dehydratase large subunit			(REC 4.2.1.33)	Putative 3-isopropylmalate dehydratase large subunit
NCBI_TaxID=65699;	NCBI_TaxID=65699;			NCBI_TaxID=65699;	NCBI_TaxID=65699;			NCBI_TaxID=65699;	NCBI_TaxID=65699;
SEQUENCE FROM N.A.	SEQUENCE FROM N.A.			SEQUENCE FROM N.A.	SEQUENCE FROM N.A.			SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
STRAITAN-Z2991 / SEROGROUP A / SEROTYPE 4A.	STRAITAN-Z2991 / SEROGROUP A / SEROTYPE 4A.			STRAITAN-Z2991 / SEROGROUP A / SEROTYPE 4A.	STRAITAN-Z2991 / SEROGROUP A / SEROTYPE 4A.			STRAITAN-Z2991 / SEROGROUP A / SEROTYPE 4A.	STRAITAN-Z2991 / SEROGROUP A / SEROTYPE 4A.
Leuc.; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.	Leuc.; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.			Leuc.; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.	Leuc.; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.			Leuc.; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.	Leuc.; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

RX	MEDLINE=20222556; PubMed=10761919;
RA	Parikh J., Fichtman M., James K.D., Bentley S.D., Churcher C.,
RA	Klie S.R., Morelli G., Brown D., Chillingworth T.,
RA	Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA	Jagels K., Leather S., Moule S., Mongall K., Quail M.A.,
RA	Rajandream M.A., Rutherford K.M., Simmonds M., Skeilton J.,
RA	Whitehead S., Spratt B.G., Barrell B.G.,
RT	"Complete DNA sequence of a serogroup A strain of <i>Neisseria meningitidis</i> 2491."
RT	RL
DR	EMBL; AL162756; CAB84686.1;
DR	InterPro; IPR01030; Aconitase_N.
DR	InterPro; IPR004430; LeuC.
DR	PFam; PF00330; aconitase_1.
DR	PRINTS; PR00415; ACONITASE.
DR	ProDom; PD000511; Aconitase_N; 1.
DR	TIGRFAMS; TIGR00170; lacC; 1.
DR	PROSITE; PS00050; ACONITASE_1;
DR	PROSITE; PS01244; ACONITASE_2;
KW	Lyase; Complete proteome.
SEQUENCE	469 AA; 5073 MW; 89AB349827DA25DB CRC64;
Query	38 1%; Score 1545.5; DB 16; Length 469;
Best Local Similarity	63.4%; Pred. No. 4.2e-96;
Matches	301; Conservative 62; Mismatches 103; Indels 9; Gaps 3
Qy	7 TPTOTLYDKVLOAHVYDEKLGDGTPTVLLYIDRHLVHEVTSPQAPEGRLNAGKVRPDPCTLAT 66
Db	2 TAQTLYDKLWNHIVVREEDGTVLLYIDRHLVHEVTSPQAPEGRLNAGKVRPDPCTLAT 61
Qy	67 TDHNVPITSRKALKDIASSKEDDSRTQCVTLEENVKEFG-VTYFGSLSDKRGQIVHVG 125
Db	62 ADINTPT --- - GDWDKCIQDPISKLQVDTLDKNIKEFGALAYFFPMDKSGQIVHVG 115
Qy	126 EQGFTLPGTTVVGDSHTSHTGAGALAGIGTSEVHIAQTCLTRKSXNMTRIQVDE 185
Db	116 EQGATLPGMTVVGDSHTSHTGAGALAGIGTSEVHIAQTCLTRKSXNMTRIQVDE 175
Qy	186 LAPGVISSKKVVLHAIGIIGTAGGTGAVIIFCGSVIRSLSMEARMSCTNMSIEGGARAGM 245
Db	176 LIKAGVTAQDVALIYIGQITAGGTGYAIFRGGEATRSLSGEGRMTLNCNAAGM 235
Qy	246 APDEITPEYIKGRPLAKYDSDPEWKHAKTYQWNKLQSDPGAKYDIDVFDIAKDIVPILTWG 305
Db	236 AVDQTTIDYKDKPFAPEGEA -- WDKAKEYWRTLVSDEGAVFDKEYRNAEDIEPQVW 293
Qy	306 TSPEDVVPITGVVPDPETPATEAKKADGFRMLQYNGLKAGTPMEDIPVDKVYFIGSCTNSR 365
Db	294 TSPEMVLDISSKVNPAAETDPYKRSQMERALEWGLEATPLNEIPDVIPIGSCTNSR 353
Qy	366 TEDLRAAAAVVKGRKKPAVNKSAMVPGSGLVKTOAEEGLDKIPEEAGFEEWREAGCSMC 425
Db	354 VEDLREAAAIAKDRKKAAANQVRLIVPGSGLVRKQAEKGLDKIPEEAGFEEWREAGCSMC 413
Qy	426 LGMNPDLAQPQERCASTSNRNFEGROGAGGRHLMSPVMAAGIYVKLADVRK 480
Db	414 LAMNADRLTPGQRCASTSNRNFEGROGNGGRTHLVSPAAAAYVGRFTDIRMM 468
RESULT 10	
Q9HZAA3	PRELIMINARY;
ID	PRT;
Q9HZAA3	PRELIMINARY;
AC	PRT;
Q9HZAA3	474 AA.
DT	01-MAR-2001 (TREMBLrel. 16, Created)
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE	3-isopropylmalate dehydratase large subunit
GN	LEUC OR PA3121.
OS	<i>Pseudomonas aeruginosa</i> .
OC	Bacteria; Proteobacteria; gamma subdivision: <i>Pseudomonadaceae</i> ;
OC	<i>Pseudomonas</i> .
ON	NCBI_TaxID=287;
ON	NCBI_TaxID=11.

RP SEQUENCE FROM N.A.  
 RC STRAINATCC 15692 / PA01;  
 RX MEDLINE=20437337; PubMed=0984043;  
 RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P.,  
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,  
 RA Barber R.L., Goitier S.N., Folger K.R., Kas A., Larbig K., Lin R.M.,  
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lin R.M.,  
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
 RA Reizer J., Saier M.H., Hancock R.E.W., Iory S., Olson M.V.;  
 RT "Complete genome sequence of *Pseudomonas aeruginosa* PA01, an  
 opportunistic pathogen";  
 RL Nature 406:959-964(2000).  
 EMBL: AE004736; AAG0509.1; --.  
 InterPro: IPR001030; Aconitase\_N.  
 IntPro: IPR00430; LeuC.  
 Pfam: PF00330; aconitase\_1.  
 PRINTS: PRO0415; ACONITASE.  
 PRODOM: PDO0051; Aconitase\_N; 1.  
 TIGRFAMS: TIGR00170; leuC; 1.  
 PROSITE: PS00050; ACONITASE\_1; 1.  
 PROSITE: PS01244; ACONITASE\_2; 1.  
 KW Complete proteome.  
 SEQUENCE 474 AA; 51042 MW; 7B4A0F6500C228BC CRC64;

Query Match 37.2%; Score 1507.5; DB 16; Length 474;  
 Best Local Similarity 62.5%; Pred. No. 1.6e-93; Indels 113; Mismatches 3; Gaps 2;  
 Matches 295; Conservative 61; Mismatches 113; Indels 3; Gaps 2;

QY 9 QTYLKDVLQAHVDEKLDGTWLYLIVYDRLHVEHTSQAEGFLRNAGRKVRPDTLTD 68  
 Db 4 KTYLKDVLQAHVDEKLDGTWLYLIVYDRLHVEHTSQAEGFLRNAGRKVRPDTLTD 63  
 QY 6 9 HNVPTTSRKALKDIASTIKEDDSRTQCVTLEENKVEFGVTWGLSDKRGVQGIVHVGPEQ 128  
 Db 6 4 HNVPTTSRKALKDIASTIKEDDSRTQCVTLEENKVEFGVTWGLSDKRGVQGIVHVGPEQ 122  
 QY 129 FTLPGTTWVGDSHTSHTGARGALAGIGTSEVHEVIAOTCLTKESKNMRTOVDBELAP 188  
 Db 123 ATLPGMWVCGDSHTSHTGARGALAGIGTSEVHEVIAOTCLVKMKMVLVGEGRPLA 182  
 QY 189 GVS SKVWVLHAGIGTGGTCAVIEFCGSVIRSLSMEARMSICNNSIEGGRAGRMVAD 248  
 Db 183 GVTAKDVLAVLAVIGRIGTGGTCAVIEFCGSVIRSLSMEARMSICNNSIEGGRAGRMVAD 242  
 QY 249 EITFEVYKGRPLAKPVYDPSWIKATQWKNLQSDPGKAYDIDVFDIADKIVPTLWTGTPSP 308  
 Db 243 OKTIDVYKGRPPA- SAEQNDQAVACWQGLVSDADARFDTVELDAQKPVQSVNGTSP 300  
 QY 309 EDVYPTIGVWVDPDPETRATTEAKKADGRMLQWGLKAGTPMDIPVDKVFLGSCTNRIED 368  
 Db 301 ENVLAVDNOVDPDAPRESDDPIKGSTERALKWGLRPNQAITDQLQFVFLSCTNSRIED 360  
 QY 369 LRAAAVWKGKKAPNUTSAMVPGSIVVKTQAEEGDLDKIFEEAGFWRERENGCSMLGM 428  
 Db 361 LRAAAEVARGKVAATIKOALWPGSIVVKTQAEEGDLDKIFEEAGFWRERENGCSMLGM 420  
 QY 429 NPDILAPCERCASTSNRNFEGSROGAGERTHIMSPVMAAAGIVGKLAQVRL 480  
 Db 421 NPDRLSEGGCASTSNRNFEGSROGAGERTHIMSPVMAAAGIVGKLAQVRL 472  
 RESULT 11  
 QPAX0 PRELIMINARY; PRT; 474 AA.  
 OPPAX0; PRELIMINARY; PRT; 474 AA.  
 AC OPPAX0;  
 DT 01-OCT-2000 (TREMBrel. 15, Created)  
 DT 01-OCT-2000 (TREMBrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)  
 DE 3-isopropylmalate dehydratase large subunit.  
 GN XP2375.  
 OS *Xylella* fastidiosa.  
 OS *Xylella*, *Proteobacteria*; gamma subdivision; *Xanthomonas* group;  
 OC *Xylella*.

OX NCBI\_TaxID=2371;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=9A5C;  
 RX SIMPSON A.J.G., Reineach F.C., Arruda P., Abreu F.A., Acencio M.,  
 RA Alvarango R., Alves L.M.C., Araya J.E., Borda G.S., Bapista C.S.,  
 RA Barros M.H., Bonacorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,  
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,  
 RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,  
 RA Coutinho U.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,  
 RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,  
 RA Fraga J.S., Franca S.C., Franco M.C., Frohne M., Furian L.R.,  
 RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,  
 RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,  
 RA Krieger J.E., Kuramae E.E., Laigret F., Lemos M.R., Leite L.C.C.,  
 RA Lemos E.G.M., Lemos M.V.P., Lopes C.R., Machado J.A.,  
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,  
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,  
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorcello C.B.,  
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,  
 RA Nhani A.Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,  
 RA Oliveira M.C., Oliveira R.C., Palmeri D.A., Paris A.,  
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,  
 RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,  
 RA Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawaaki H.E.,  
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,  
 RA da Silveira J.F., Silvestri M.I.Z., Siqueira S.M., de Souza A.A.,  
 RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,  
 RA Zago M.A., Zatz M., Meidanis J., setubal J.C.;  
 RT "The genome sequence of the plant pathogen *Xylella fastidiosa*";  
 RL Nature 406:151-159 (2000).  
 DR EMBL: AE003047; AAF83174.1; --.  
 DR InterPro; IPR001030; Aconitase\_N.  
 DR InterPro; IPR00430; LeuC.  
 DR PR00330; aconitase\_1.  
 DR PRINTS; PRO0415; ACONITASE.  
 DR PRODOM; PDO0051; Aconitase\_N; 1.  
 DR TIGRFAMS; TIGR00170; leuC; 1.  
 DR PROSITE; PS00050; ACONITASE\_1; 1.  
 DR PROSITE; PS01244; ACONITASE\_2; 1.  
 KW Complete proteome.  
 SEQUENCE 474 AA; 51183 MW; 998D5FDFB2B23750 CRC64;

Query Match 37.0%; Score 1498.5; DB 16; Length 474;  
 Best Local Similarity 63.1%; Pred. No. 6.4e-93; Indels 119; Mismatches 119; Gaps 3; Gaps 2;  
 Matches 298; Conservative 52; Mismatches 119; Indels 3; Gaps 2;

QY 9 QTYLKDVLQAHVDEKLDGTWLYLIVYDRLHVEHTSQAEGFLRNAGRKVRPDTLTD 68  
 Db 4 KTYLKDVLHIEVARRDGSSLYLIVDRLHVEHTSQAEGFLRNAGRKVRPDTLTD 63  
 QY 69 HNVPTTSRKALKDIASTIKEDDSRTQCVTLEENKVEFGVTWGLSDKRGVQGIVHVGPEQ 128  
 Db 64 HNVPTTSRKALKDIASTIKEDDSRTQCVTLEENKVEFGVTWGLSDKRGVQGIVHVGPEQ 122  
 Db 123 ATLPGMWVCGDSHTSHTGARGALAGIGTSEVHEVIAOTCLVKMKMVLVGEGRPLA 182  
 QY 189 GVS SKVWVLHAGIGTGGTCAVIEFCGSVIRSLSMEARMSICNNSIEGGRAGRMVAD 248  
 Db 183 GVTAKDVLAVLAVIGRIGTGGTCAVIEFCGSVIRSLSMEARMSICNNSIEGGRAGRMVAD 242  
 QY 249 EITFEVYKGRPLAKPVYDPSWIKATQWKNLQSDPGKAYDIDVFDIADKIVPTLWTGTPSP 308  
 Db 243 EITFEVYKGRPLAKPVYDPSWIKATQWKNLQSDPGKAYDIDVFDIADKIVPTLWTGTPSP 300  
 QY 309 EDVYPTIGVWVDPDPETRATTEAKKADGRMLQWGLKAGTPMDIPVDKVFLGSCTNRIED 368  
 Db 301 ENVLAVDNOVDPDAPRESDDPIKGSTERALKWGLRPNQAITDQLQFVFLSCTNSRIED 360

Qy	369	LRAAAVYVKRKKAAPNPKSAMVYPPGSLVYKTOAREGLDKIFEBAGFWEAGGSMCLGM	428	Db	295	EMVVS1EDRVPDPDKEKDPVKRNAMMERALEYMAQPNVAIGDIRDKVFIGSCTNSRIED	354
Db	361	LRAAAVYVKRKVASTVQAMVPPGSLVYKTAQAEVEGLDKIFEBAGFWEAGGSMCLAM	420	Qy	369	LRAAAVYVK--GRKKAPNPKSAMVYPPGSLVYKTOAREGLDKIFEBAGFWEAGGSMCL	426
Qy	429	NPDILAPQERCASTSNRNPFGQAGGRTLMSPVMAAGIVGKLVADYKL	480	Db	355	MRAAAWVQQLGKRIASNVKLMVPGSLVYKTOAREGLDKIFEBAGFWEAGGSMCL	414
Db	421	NPDKLGSSEHCASTSNRNPFGQJGRTLVSFAMAAAAVAGHFVDFREM	472	Qy	427	GMNPDPDLPQERCCASTSNRNPFGQAGGRTLMSPVMAAGIVGKLVADYKL	480
				Db	415	AMNADLPLEPGERCASTSNRNPFGQAGGRTLVSFAMAAAALLEGHFVDFVRL	468
<b>RESULT 12</b>							
Q8XXXX3		PRELIMINARY;		PRT;	469	AA.	
AC	Q8XXXX3;						
DT	01-MAR-2002	(TREMBLrel.	20, Created)				
DT	01-JUN-2002	(TREMBLrel.	21, Last annotation update)				
DE	Probable 3-isopropylmalate dehydratase (Large subunit)	protein					
GN	LEUC	OR RSC1990	OR RS01558.				
OS	Ralstonia solanacearum	(Pseudomonas solanacearum)					
OC	Bacteria; Proteobacteria; beta subdivision; Ralstonia	group;					
NCBI_TaxID=305;							
OX							
RN							
RP	SEQUENCE FROM N.A.						
RC	STRAIN=GMI1000;						
RX	MEDLINE=211681879; PubMed=11823852;						
RA	Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,						
RA	Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,						
RA	Chandler M., Choine N., Claude-Renard C., Cunnac S., Demange N.,						
RA	Gaspin C., Lavia M., Moisan A., Robert C., Saurin W., Schilex T.,						
RA	Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,						
RA	Weissenbach J., Boucher C.A./						
RT	"Genome sequence of the plant pathogen Ralstonia solanacearum."						
RL	Nature 45:497-502(2002).						
DR	InterPro: IPR001030; CAD15692;1; -						
DR	InterPro: IPR04430; Leuc.						
DR	InterPro: IPR04430; Leuc.						
DR	PRINTS: PR00330; aconitase; 1.						
DR	P-TERM: PR00415; ACONITASE.						
DR	P-DOM: PD00051; Aconitase_N; 1.						
DR	TIGRFAMS: TIGR00101; Leuc; 1.						
DR	PROSITE: PS00450; ACONITASE_1; 1.						
DR	PROSITE: PS01244; ACONITASE_2; 1.						
KW	Lysase; Complete proteome.						
SEQUENCE	469 AA; 50796 MW;	B451E96E44788AAE	CRC64;				
Query Match	36.8 %	Score 1493;	DB 16;	Length 469;			
Best Local Similarity	63.5 %	Pred. No. 1..5e-92;					
Matches 301; Conservative	53;	Mismatches 110;	Indels 10;	Gaps 3;			
Qy	9	QTYLYDKVLOQAHVYDEKLDTGVLVYIDRHLVHEYTSPOAFAEGLNAGRKVYRDPCTLATTID	68	Db	63	HNVPTTDR----SHGLADPVSKVQVDTLADNCDSFGITQFQMTDKRQGTVHVGPEQG	128
Db	3	KTYLYKLWDDHVWHTEDDTGTVYIDRQLHEVTSPOAFAEGLNRPWIRISNALVSD	62	Qy	69	FILPGTIVVCGDSHTSHTGAGLAFGIGTSEVHVLATQCLLTAKSKNMRIQVGDGELAP	116
Qy	129	HNVPTTSRKALDKIASFIKEKDSRTQCVTLLENTKEVYFGTISLDSKROGTVHVGPEQG	128	Db	63	ATLPGMTVUCGDSHTSHTGAGLAFGIGTSEVHVLATQCLLTAKSKNMRIQVGDGELAP	188
Db	117	ATLPGMTVUCGDSHTSHTGAGLAFGIGTSEVHVLATQCLLTAKSKNMRIQVGDGELAP	176	Qy	189	GYSSKDQVVLHAGLIGTGTAGGTGAVIEFGCSVIRSLSMARMSICNMSTEGGARAGMVPD	248
Qy	189	GYSSKDQVVLHAGLIGTGTAGGTGAVIEFGCSVIRSLSMARMSICNMSTEGGARAGMVPD	248	Db	177	GCTAKD1VLA1GKTAGGTGAMERGCSA1RALSMGRMTVCNMA1EAGARAGMVGVD	236
Db	177	GCTAKD1VLA1GKTAGGTGAMERGCSA1RALSMGRMTVCNMA1EAGARAGMVGVD	236	Qy	249	EITFEYLGKGRPLAKPKDSPEWPKHATQYKWNQLQSDPGAKYIDVFDIDVPLTWGTS	308
Qy	249	EITFEYLGKGRPLAKPKDSPEWPKHATQYKWNQLQSDPGAKYIDVFDIDVPLTWGTS	308	Db	237	DITLEYLKGRPPAFOQ--GWEVQAVYRSLSHDEGARFDHVYELRAEIRPQSWGTSP	294
Db	237	DITLEYLKGRPPAFOQ--GWEVQAVYRSLSHDEGARFDHVYELRAEIRPQSWGTSP	294	Qy	309	EDVVPITGVVPPDPETFATEAKKADGRMRMLQYMGKAGTPMEDIPIVDKVFISCTNSRIED	368
Qy	309	EDVVPITGVVPPDPETFATEAKKADGRMRMLQYMGKAGTPMEDIPIVDKVFISCTNSRIED	368	Db	129	FTLPGTIVVCGDSHTSHTGAGLAFGIGTSEVHVLATQCLLTAKSKNMRIQVGDGELAP	188
<b>RESULT 13</b>							
Q8XA00		PRELIMINARY;		PRT;	466	AA.	
AC	Q8XA00;						
DT	01-MAR-2002	(TREMBLrel.	20, Created)				
DT	01-MAR-2002	(TREMBLrel.	20, Last sequence update)				
DE	Probable 3-isopropylmalate isomerase (dehydratase) subunit.						
GN	LEUC	OR RSC1990	OR ECS0076.				
OS	Bacteri	Escherichia coli O157:H7.					
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;						
OC	Escherichia.						
OX							
NCBI_TaxID=83334;							
RN							
RP	SEQUENCE FROM N.A.						
RC	SEQUENCE FROM N.A.						
RX	SEQUENCE FROM N.A.						
RC	SEQUENCE FROM N.A.						
RX	SEQUENCE FROM N.A.						
RC	SEQUENCE FROM N.A.						
RX	SEQUENCE FROM N.A.						
RC	SEQUENCE FROM N.A.						
RX	SEQUENCE FROM N.A.						
RC	SEQUENCE FROM N.A.						
RX	SEQUENCE FROM N.A.						
RA	Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,						
RA	Han C.-G., Ohtsubo E., Nakayama K., Murata M., Tobe T., Tanaka M., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,						
RA	Iida T., Takami H., Hattori M., Shinagawa H., Dimalanta E.T., Potamousis K.,						
RA	Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,						
RA	Welch R.A., Blattner F.R.,						
RT	"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7;"						
RL	Nature 403:529-533 (2001).						
RL	[12]						
RP	SEQUENCE FROM N.A.						
RC	SEQUENCE FROM N.A.						
RX	SEQUENCE FROM N.A.						
RC	SEQUENCE FROM N.A.						
RX	SEQUENCE FROM N.A.						
RA	Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,						
RA	Han C.-G., Ohtsubo E., Nakayama K., Murata M., Tobe T., Tanaka M., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,						
RA	Iida T., Takami H., Hattori M., Shinagawa H., Dimalanta E.T., Potamousis K.,						
RA	Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,						
RT	"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12."						
RL	DNA Res 8:11-22 (2001).						
DR	AE00184; AAG51376;1; -						
DR	EMBL; AP002550; BAB31499;1; -						
DR	InterPro; IPR01030; Aconitase_N.						
DR	InterPro; IPR04430; aconitase; 1.						
DR	PRINTS; PR00330; aconitase.						
DR	P-TERM; PR00415; ACONITASE.						
DR	TIGRFAMS; TIGR00170; leuC_I.						
DR	PROSITE; PS00450; ACONITASE_1.						
DR	PROSITE; PS01244; ACONITASE_2.						
KW	Isomerase; Complete proteome.						
SEQUENCE	469 AA; 49898 MW;						
Query Match	36.2 %	Score 1469.5;	DB 16;	Length 466;			
Best Local Similarity	61.9 %	Pred. No. 5.6e-91;					
Matches 292; Conservative	59;	Mismatches 112;	Indels 9;	Gaps 4;			
Qy	9	QTYLYDKVLOQAHVYDEKLDTGVLVYIDRHLVHEYTSPOAFAEGLNAGRKVYRDPCTLATTID	68	Db	3	KTYLYKLWDDHVWHTEDDTGTVYIDRQLHEVTSPOAFAEGLNRPWIRISNALVSD	62
Qy	69	HNVPTTSRKALDKIASFIKEKDSRTQCVTLLENTKEVYFGTISLDSKROGTVHVGPEQG	128	Db	69	HNVPTTSRKALDKIASFIKEKDSRTQCVTLLENTKEVYFGTISLDSKROGTVHVGPEQG	128
Db	63	ATLPGMTVUCGDSHTSHTGAGLAFGIGTSEVHVLATQCLLTAKSKNMRIQVGDGELAP	116	Qy	63	HNVS1CT---KDINAC- -GEMARIQMQLIKNCRFGEVLYDNPMPYQG1VHVMGPBQG	116
Qy	129	FTLPGTIVVCGDSHTSHTGAGLAFGIGTSEVHVLATQCLLTAKSKNMRIQVGDGELAP	116	Db	129	FTLPGTIVVCGDSHTSHTGAGLAFGIGTSEVHVLATQCLLTAKSKNMRIQVGDGELAP	188

Db 117 VTLPGMTIVCGSDHTATHGAFALAFAGTGTSEVHVLATQVLTQKGRAKTMKTEVQGKAP 176  
 Qy 189 GVSSKDVWTHAIGIITAGGTGAVIEPGSVRSLNEMARNSICNSIEGGRAGMYPD 248  
 Db 177 GITAKDVLVLAIGKTLSAGGTGHVPERGEATRDLNEMGRMTLNCNALEMGAKAGLVPD 236  
 Qy 249 EITPEVYKGRPLAKYDPEWVKATQWKNLQSDPGAKYDIDVFDKDIVPLTNGSP 308  
 Db 237 ETTENVYKGRLHAPK- GKDFDAVWKTLODEGATFDVTWLOREIISPOVTWNTP 294  
 Qy 309 EDVVPITGVVDPDPEFAEAKAGDGRMLQYMGKAGTPMEDIPVDKVFIISCTNRIED 368  
 Db 295 GQVISVNDNIPDPAFDPVERAEGKALAYWGLKPGILITVAIDKVFISCTNSKED 354  
 Qy 369 LRAAAVVKGRKAKPNVSKAMTYPGSKVLTQAEEDLKFEEAGFWRAGCSCMIGM 428  
 Db 355 LRAAAEAKGRKAVPGVQ- ALIVPGSGPKAQAEGLDIFTEAGFWRULPGCSMCLAM 413  
 Qy 429 NPDILAPQERCASNRNFEGROGAGGRTHLMSPVMAAAGIVGKLAQVKL 480  
 Db 414 NNDRLNPGERCASNSNFEGROGSGRTHLVSPAMAAAATVGHFADIRN 465  
 RESULT 14  
 08ZIHO ID Q8ZIHO PRELIMINARY; PRT; 476 AA.  
 AC 08ZIHO:  
 DT 01-MAR-2002 (TREMBLREL. 20, Last sequence update)  
 DT 01-MAR-2002 (TREMBLREL. 20, Last annotation update)  
 DE 3-isopropylmalate dehydratase large subunit (EC 4.2.1.33).  
 GN LBUUC OR YP01531.  
 OS Vervinia pestis.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 Vervinia.  
 OX NCBI\_TaxID=632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CO-92 / BLOVAR ORIENTALIS;  
 RX MEDLINE=21470413; PubMed=1586360;  
 RA Chillingworth T., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,  
 Prentice M.B., Sebaiha M., James K.D., Churcher C., Mungall K.L.,  
 Baker S., Basham D., Bentley D.S., Brooks K., Cerdeno-Tarago A.M.,  
 Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,  
 Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,  
 Leather S., Moule S., Oyston P.C.F., Quail M., Rutledge J.,  
 Simmonds M., Skeatley J., Stevens K., Whitehead S., Barrell B.G.;  
 RT "Genome sequence of *Vervinia pestis*, the causative agent of plague.". Nature 413:523-527 (2001).  
 RL Nature 413:523-527 (2001).  
 DR SMBL; AU41413; CAC89388.1; --.  
 DR InterPro; IPR001030; Aconitase\_N.  
 DR InterPro; IPR004430; LeuC.  
 DR Pfam; PF00330; aconitate; 1.  
 DR PRINTS; PR00415; ACONITASE.  
 DR PRODOM; PD00051; Aconitase\_N; 1.  
 DR TIGRFAM; TIGR00170; LeuC; 1.  
 DR PROSITE; PS00450; ACONITASE\_1; 1.  
 DR PROSITE; PS01244; ACONITASE\_2; 1.  
 DR KW Lyase; Complete proteome.  
 SQ SEQUENCE 476 AA; 50589 MW; 052D8EB2165F5E74 CRC64;  
 Query Match 35.8%; Score 1452; DB 16; Length 476;  
 Best Local Similarity 59.2%; Pred. No. 8.98-90;  
 Matches 289; Conservative 66; Mismatches 121; Indels 12; Gaps 5;  
 Qy 1 MIGAESTHTQTYKVKLQHVDKLDGTWLYDRLHTEVTSPOAFCFLNAGKVRP 60  
 Db 1 MGTTSSORTKLYQKLYDHLVHAPNETPPLYIDRLHTEVTSPOAFCFLNAGKVRP 60  
 Qy 61 DCLLATPPHNPVPTSKALKDIAPIKDSRQCYTLEENVEKFGVYFLGSLDKRCIV 120  
 Db 61 GKTFTAMDHNVSTOT---KDINA--SEBMARIQMQLKNCABFGVSYLYDLMHFOCIV 114

Qy 121 HVTGPEQGFTLPGTIVCGSDHTSTHGAFGALAFAGTGTSEVHVLATQVLTQKGRAKTMKTEVQGKAP 180  
 Db 115 HVIGPEQGFTLPGMTIVCGSDHTATHGAFGSLAFIGTSEVHVLATQVLTQKGRAKTM 174  
 Qy 181 QVTGELAPGVSSKDVWTHAIGIITAGGTGAVIEPGSVIISLMEARNSICNSIEGGRAGMYPD 240  
 Db 175 EYNGTVGAGITAKDVLVLAIGKTLSAGGTGHVPERGEATRDLNEMGRMTLNCNALEMGA 234  
 Qy 241 RAGMVADEITEVYKGRPLAKYDPEWVKATQWKNLQSDPGAKYDIDVFDKDIVP 300  
 Db 235 KAGIVNAPDDTIFALKERQRQFAP- -TGEQWEGQVAYMRTLKSADAQDTIVLDAADIAP 292  
 Qy 301 TLTWIGISPEDWVPTGVVDPDPEFAEAKAGDRMLQYMGKAGTPMEDIPVDKVFIGS 360  
 Db 293 QVWGTNPQVQIAVNOITPAPESPSPDVERAEGKALAYMDLRPGKLTVEAIDKVFIS 352  
 Qy 361 CTNSRIEDLRAAAVVKGRKAKPNVSKAMTYPGSLVLTQABEEGLDKIFEEAGFEEREA 420  
 Db 353 CTNSRIEDLRAAAVAKGRKAVPGVQ- ALIVPGSGPKAQAEGLDIFTEAGFWRULP 411  
 Qy 421 GCSMCLGKHNPDILAPQERCASNRNFEGROGAGRTHLMSPVMAAAGIVGKLAQVKL 480  
 Db 412 GCSMCLAMNDRLEPGERCASNSNFEGROGSGRTHLVSPAMAAAATVGHFADIREL 471  
 Qy 481 TDYKASPH 488  
 Db 472 S--ATH 476  
 RESULT 15  
 QKRP81 ID QKRP81 PRELIMINARY; PRT; 467 AA.  
 AC QKRP81:  
 DT 01-OCT-2000 (TREMBLREL. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBLREL. 15, Last annotation update)  
 DE 3-isopropylmalate dehydratase, large subunit.  
 GN VCA492.  
 OS Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.  
 OC NCBI\_TaxID=666;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=EL TOR NT\_06961 / SEROTYPE 01;  
 RX MEDLINE=20406833; PubMed=10952301;  
 RA Heidelberg J., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,  
 Douson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,  
 Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,  
 Rmalaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,  
 McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,  
 Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,  
 RA Fraser C.M.,  
 RT "DNA sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*". Nature 406:477-483 (2000).  
 RL Nature 406:477-483 (2000).  
 DR EMBL; AE004318; AAH95634.1; --.  
 DR TIGR; VC2492; --.  
 DR InterPro; IPR001030; Aconitase\_N.  
 DR InterPro; IPR004430; LeuC.  
 DR Pfam; PF00330; aconitate; 1.  
 DR PRINTS; PR00415; ACONITASE.  
 DR PRODOM; PD00051; Aconitase\_N; 1.  
 DR TIGRFAM; TIGR00170; LeuC; 1.  
 DR PROSITE; PS00450; ACONITASE\_1; 1.  
 DR PROSITE; PS01244; ACONITASE\_2; 1.  
 DR KW Complete proteome.  
 DR SEQUENCE 467 AA; 50185 MW; 4F760714FA85ADD CRC64;

Query Match 35.2%; Score 1425.5; DB 16; Length 467;  
 Best Local Similarity 58.9%; Pred. No. 5.38-88;  
 Matches 279; Conservative 67; Mismatches 119; Indels 9; Gaps 4;

Qy	6	STPOTLYDKVLOAHVVDKLDGTIVLLYIDRHLHYEVTSPQAFFGLRNAGKVRPRPCTLA	65
Db	2	SKARTLYEKIYDHAHVVVAAPGETPILYIDRHLHYEVTSPQAFFGLRNAGKVRPRPCTLA	61
Qy	66	TDHNVPPTSALKDIAFKEKDDSRQCVTLEENVKEFGTYFGLSDKROGTVHVGTP	125
Db	62	TMDHNVSITT----KDINA---SGEMARLQMTLSKNCCEFFGTVLTDINHXYGIVHNGP	115
Qy	126	EGCFTLPETTWCDDSHPSTHGATGALFGTGTSEVILATOLITRKSKNRIVQDVE	185
Db	116	ELGITLPMTIVCGDSHTATHGAFGLAFTGIGTSEVILATQTLQGRAKTMKIEVRGK	175
Qy	186	LAPGVSSKDVVLAHAIGLITGAGTGTGAVTEFGSVIRSLSMEMRSICMNSIEGGRAGMV	245
Db	176	VAGITARDIVLAIGKTTAEGTGYVEFGEAIRDLSMEGRMTVCNNAELGAGLI	235
Qy	246	ADDEITPFLKGRLPLAKYDPSPEWKAQTYWNLQSDPGAKYDIDVFDKDVPTLTWG	305
Db	236	APPATTFVYKGRKFKAPO--GSDWDAADVWQTLKTDDEAQDAVVTLEASELKPOVTWG	293
Qy	306	TSEDWVBITGVPDPETTAEAKKADGRMLQYMGKAGTGFMDIPDVFKVFTGSCTNSR	365
Db	294	TNGQVIAVDEPPPSQFADPVERSSAKALAYMGLEGKMLSDYKDVFKVFTGSCTNSR	353
Qy	366	IEPLRAAAAVVKGKKAQPKVNSAMVPPGSGLYKTCQAERGLDK1FEEAGFENREAGCSMC	425
Db	354	IEPMRAAAAVVKGKKAQPKVNSAMVPPGSGLYKTCQAERGLDK1FEEAGFENREAGCSMC	412
Qy	426	LGMPNDLAPQERCASTSNRNFGRQGGRTHLMSPVMAAAGIVGKLAQDVR	479
Db	413	LAMNNDRIGPGERCASTSNRNFGRQGGRTHLVSPPAMAALAAIAGHFVDVR	463

## RESULT 16

Q9K8F0	PRELIMINARY;	PRT;	472 AA.
AC	Q9K8F0;		
DT	01-OCT-2000	(TREMBLrel. 15, Created)	
DT	01-JUN-2002	(TREMBLrel. 15, Last sequence update)	
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)	
DE	3-isopropylmalate dehydratase large subunit.		
DE	LEUC OR BH3056.		
OS	Bacillus halodurans.		
OC	Bacteria; Firmicutes; Bacteriia; Actinobacteria; Actinomycetales; Streptomyces; Streptomyces; Streptomyces.		
OC	NCBI_TaxID=1902;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=A3 (2);		
RA	Murphy L., Harris D.		
RL	Submitted (JUL-1998)		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=A3 (2);		
RA	Murphy L., Harris D.		
RL	Submitted (JUL-1998)		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=A3 (2);		
RA	Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S., Rabinowitz B., Rajandream M.A., Rutherford K., Rutter S.,		

Query Match 34.4%; Score 1396; DB 16; Length 472;  
Best Local Similarity 59.2%; Prod. No. 5.3e-86;  
Matches 279; Conservative 58; Mismatches 124; Indels 10; Gaps 3;

8 POTLYDKVLOAHVVDKLDGTIVLLYIDRHLHYEVTSPQAFFGLRNAGKVRPRPCTLA



DR	InterPro; IPR01030; Aconitase_N.	DR	PRINTS; PRO0415; ACONITASE.
DR	InterPro; IPR00430; LeuC.	DR	ProDom; PD000511; Aconitase_N; 1.
DR	PF00330; aconitase; 1.	DR	TIGRFAMS; TIGR00170; leuC; 1.
DR	PRINTS; PRO0415; ACONITASE.	DR	PROSITE; PS00450; ACONITASE; 1.
DR	ProDom; PD000511; Aconitase_N; 1.	DR	PROSITE; PS01244; ACONITASE_2; 1.
DR	TIGRFAMS; TIGR00170; leuC; 1.	KW	Plasmid.
DR	PROSITE; PS00450; ACONITASE; 1.	FT	NON-TER.
DR	PROSITE; PS01244; ACONITASE_2; 1.	FT	448
KW	Isomerase; Plasmid.	SQ	SEQUENCE 448 AA; 49936 MW; 0137DA4418C29779 CRC64;
SEQUENCE	469 AA; 52426 MW; 4094EC232646228B CRC64;	Query Match	33.4%; Score 1354; DB 2; Length 469;
Best Local Similarity	56.6%; Pred. No. 3.6e-33;	Best Local Similarity	32.4%; Score 1315.5; DB 2; Length 448;
Matches	267; Conservative 76; Mismatches 119; Gaps 5;	Matches	57.1%; Pred. No. 1.3e-80;
Db	3 KTLKDIYDHHVIEEKNNNISLYDLHLHEVTSQAFSLRMNRSVQPKCTFATMD 62	Db	260; Conservative 70; Mismatches 116; Gaps 4;
Qy	69 HNVPTTSRKALKDIASTFIKEKDDSRTOCYTLEENYKEFGVTVYFGSLDKRQGIVHVGPEQ 128	Qy	9 QTLQDKVLQAHVYDVEKLDGTVLILYDRLHVETHVTSQAFGLRNAGRKVVRPDCTLATTD 68
Db	63 HNVSTTS---KDDNA---SSMSAKIQMQLQJINCKCBEFTIAYDINNPKQGIVHVGPEQ 116	Db	3 KTLKDIYDHHVIEEKNNNISLYDLHLHEVTSQAFSLRMNRSVQPKCTFATMD 62
Qy	129 FTLPGTTVYCGDSHTSTHGFAGLAFGIGSEVEHVLATQCLLTKRSKMRQIVDGE LAP 188	Qy	69 HNVPTTSRKALKDIASTFIKEKDDSRTOCYTLEENYKEFGVTVYFGSLDKRQGIVHVGPEQ 128
Db	117 LTLPSSTTVCGDSHTSTHGFAGLSEFGTSSEVHVLATQCLLTKQRFKMKIETGEI QK 176	Db	63 HNVSTTS---QDINA---SSMSAKVQMOPLKINQKPKCTFATMD 62
Qy	189 GVSSKDVVLHAIIGLITGAGGTGAVIEFCGGSVIRSLMSMEARSIGNMSTEGGARAGM VAPD 248	Qy	129 FTLPGTTVYCGDSHTSTHGFAGLAFGIGSEVEHVLATQCLLTKRSKMRQIVDGE LAP 188
Db	177 FITAKDILFLIGKIGLGTSSGGVIEFCGDDVTKQMMMEERTMCNMAEMGANSALI AD 236	Db	117 MTLPGMTIVCGDSHTSTHGFAGLSEFGTSSEVHVLATQCLLTKQRFKMKIETGEI QK 176
Qy	249 EITPEYLKGRLPALKYDSPWEHKRATQYWNQNLQSDPAGKVDIDYFIDAKDIVP TLWGTSP 308	Qy	189 GVSSKDVVLHAIIGLITGAGGTGAVIEFCGGSVIRSLMSMEARSIGNMSTEGGARAGM VAPD 248
Db	237 ETIYLKNNKRYSPK--NRYWDSALRYWKLTVTDNALDFKEFFDISPDISPQV TWGTSP 294	Db	177 MTLPGMTIVCGDSHTSTHGFAGLSEFGTSSEVHVLATQCLLTKQRFKMKIETGEI QK 176
Qy	309 EDVVPITGVVYVPDPETFATEAKKADGRMLQYMGMLKAGTFPMEDI PFDVKYFIGS CTNSRIED 368	Qy	249 EITPEYLKGRLPALKYDSPWEHKRATQYWNQNLQSDPAGKVDIDYFIDAKDIVP TLWGTSP 308
Db	295 DQVLISNEKIPDFNSFKDSIKDLSACNMDLKPGSYLKNIKDVKFIGS CTNSRIED 354	Db	237 EVFTSYLANKMKAFL--GIVFWKAKLNFVNLKNSDKNAFFDKVUNNISDLSPOITWGTNP 294
Qy	369 LRAAAVVKGRKAAKPVNSAMVPGSGLYKVTQABEGGLDKEFAGFEMR EACGCSMCLGM 428	Qy	309 EDVVPITGVVYVPDPETFATEAKKADGRMLQYMGMLKAGTFPMEDI PFDVKYFIGS CTNSRIED 368
Db	355 LRSAAATLKKKTSKTKI-AIVPGSGSKVNOAEKGDKIFIDAGFEWRLPGCSMCLGM 413	Db	295 DQVLISNEKIPDFNSFKDSIKDLSACNMDLKPGSYLKNIKDVKFIGS CTNSRIED 354
Qy	429 NPDLAPQERCASTSNRNFEGROGAGGRTHLMSPVMAAAGTVGKLADVRKL 480	Qy	369 LRAAAVVKGRKAAKPVNSAMVPGSGLYKVTQABEGGLDKEFAGFEMR EACGCSMCLGM 428
Db	414 NNDKLSDGERCASTSNRNFEGROGAGGRTHLMSPVMAAAGTVGKLADVRKL 464	Db	355 LRAASKLILDKKIAANNVTK-AIVPGSGSKVRAEENGLDKEFAGFEMR EACGCSMCLGM 413
RESULT	21	Q9FLW1	SEQUENCE FROM N.A.
Q9FLW1	PRELIMINARY;	PRT;	470 AA.
ID	Q9FLW1	AC	SEQUENCE FROM N.A.
AC	Q9FLW1	DT	STRAIN=NCTC 11168;
DT	01-OCT-2000 (TREMBLrel. 15, Created)	DT	MEDLINE=20150912; PubMed=10689204;
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	DT	Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C., Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S., Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W., Quail M.A., Rajandream M.A., Rutherford K.M., van Viljet A.H.M., Whitehead S., Barrell B.G.;
DE	01-JUN-2002 (TREMBLrel. 21, Last annotation update)	DE	"The genome sequence of the food-borne pathogen <i>Campylobacter jejuni</i> reveals hypervariable sequences.";
DE	Isopropylmalate dehydratase subunit (Fragment).	GN	EMBL; AL139079; CAB3703.1;
GN	LBIC.	OS	DR
OS	Buchnera aphidicola.	OC	NCBI
OC	Plasmid pLeu.	OC	InterPro; IPR001030; Aconitase_N.
OX	Bacteria; Proteobacteria; gamma subdivision; Buchnera.	OX	InterPro; IPR00430; LeuC.
RN	[1] NCBI_TaxID=9;	RN	InterPro; IPR001030; Aconitase_N.
RP	SEQUENCE FROM N.A.	RP	InterPro; IPR00330; aconitase; 1.
RC	STRAIN=NAP;	RC	InterPro; IPR00430; LeuC.
RC	MEDLINE=20576185; PubMed=11133977;	RC	InterPro; IPR001030; Aconitase_N.
RA	DT	RA	InterPro; IPR001030; Aconitase_N.
RA	01-MAR-2001 (TREMBLrel. 16, Created)	RA	InterPro; IPR00430; LeuC.
RA	01-JUN-2002 (TREMBLrel. 21, Last annotation update)	RA	InterPro; IPR001030; Aconitase_N.
RT	"Vertical transmission of biosynthetic plasmids in aphid endosymbionts (Buchnera)";	RT	InterPro; IPR001030; Aconitase_N.
RT	J. Bacteriol. 183: 785-790 (2001).	RT	InterPro; IPR001030; Aconitase_N.
RL	DR	RL	InterPro; IPR001030; Aconitase_N.
DR	AF197457; AAG31406.1;	DR	InterPro; IPR001030; Aconitase_N.
DR	InterPro; IPR001030; Aconitase_N.	DR	InterPro; IPR001030; Aconitase_N.
DR	InterPro; IPR00430; LeuC.	DR	InterPro; IPR001030; Aconitase_N.
DR	PFam; PF00330; aconitase; 1.	DR	InterPro; IPR001030; Aconitase_N.



DR	EMBL; AL59671; CAC97326.1; -.	RA	Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
DR	ListPro; LIN02096; -.	RT	"Whole genome sequencing of meticillin-resistant <i>Staphylococcus</i> aureus."
DR	InterPro; IPR001030; Aconitase_N.	RL	Lancelet; 357-1225-1240 (2001).
DR	InterPro; IPR004430; LeuC.	DR	EMBL; AP003364; BAB3146.1; -.
DR	Pfam; PF000330; aconitase_1.	DR	InterPro; IPR001030; Aconitase_N.
DR	ProDom; PD000511; Aconitase_N; 1.	DR	InterPro; IPR004430; LeuC.
DR	TIGRFAMS; TIGR00170; leuC; 1.	DR	Pfam; PF003330; aconitase_1.
DR	PROSITE; PS00450; ACONITASE_1; UNKNOWN_1.	DR	PRINTS; PR00415; ACONITASE.
DR	PROSITE; PS01244; ACONITASE_2; UNKNOWN_1.	DR	ProDom; PD000511; Aconitase_N; 1.
KW	Complete proteome.	DR	TIGRFAMS; TIGR00170; leuC; 1.
SEQUENCE	462 AA; 31041 MW; 0F09F51E77F0B4B2 CRC64;	DR	PROSITE; PS00450; ACONITASE_1.
Qy	9 QTLYDKVLOAHVVDKEDGTVLILYDRLVHEVTSPOAEGSLRNRKVRPDRDCTLATTD 68	DR	PROSITE; PS01244; ACONITASE_2; 1.
Db	3 KTLFDRLLWNHVIYGEGEPOLLYDVLHILHEVTSQAEGFLRMRERPLRFEDKTTATMD 62	KW	Complete proteome.
Qy	69 HNVPTTSRKALKDIAASFIKEDDSRQTCVTLLEVNRFQGTVYFGLSLSKRQGIVHVGPEQG 128	SEQUENCE	456 AA; 50326 MW; 4C2D584937186ECC CRC64;
Db	63 HNVPTPEDIQFQDLY-----AKQICEAQLONTQNCFFGTVLADMGSQDRQIVHMYGPETG 115	Query Match	31.6%; Score 1282; DB 16; Length 456;
Qy	129 FTLPLPTTVCGDSDHTSHTGAGLAFGIGTSEVERVHLYATOCVLTISKRNMRQVDEBLAP 188	Best Local Similarity	31.6%; Score 1282; DB 16; Length 456;
Db	116 LTOPEKVKIVCGDSDHTPAHTGAGAIGGIGSSEVEVHVFATQTIWQPKSMGIEINGLPK 175	Matches	54.4%; Pred. No. 2.5e-78;
Qy	189 GVSSKDDVLLHAIGITGAGCTGAVIEFCGSVIRSLSMEARNSICMNSIEGGARGAVAPD 248	257	Mismatches 64; Indels 20; Gaps 5;
Db	176 GVIADDDIIHLIATYGVAFGTGYAVEYGETIRNSMEERNTICNAEKGAKMGNMAPD 235	Query Match	31.6%; Score 1282; DB 16; Length 456;
Qy	249 EITPEYVLRGRPLAKYDSDPEWIKATQYKWNKLOSDPGAKYDIDVFDIAKD1VPTLTMGTSP 308	Best Local Similarity	31.6%; Score 1282; DB 16; Length 456;
Db	236 QTTPEYVGRGREYAPS----DMEKAIRDWTETLKTDDAEVOLHIEDASLLEPYVWTGTNP 291	Matches	54.4%; Pred. No. 2.5e-78;
Qy	309 EDVVPITGVVPDPETFATEAKKADGRMRMLQYMLKAGTGPMDIPVYDVKVFIGSCNTNSRIED 368	25	Mismatches 64; Indels 20; Gaps 5;
Db	292 EMGVPFSSKAFP-----EIKDMVYRAYEYVMGLKPGQTAEIEELGYVFIGSCNTNARLSD 344	Query Match	31.6%; Score 1282; DB 16; Length 456;
Qy	369 LRAAAATVKGKRAKAPNVIKSAMVVPGSKGLYKTOAEGEGLDK1FEEAGFENREAGCSMCLGM 428	Best Local Similarity	31.6%; Score 1282; DB 16; Length 456;
Db	345 LEEAATVAGNKKVNNR-ALVVPERSQVRNAAEAIGLDFKFDQFENREAGCSMCLGM 403	Matches	54.4%; Pred. No. 2.5e-78;
Qy	429 NPDILAPQERCASNSNRNFEGRQGAGGRTHLMSPMAAAAGIVGKLAIVRK 479	2	Mismatches 64; Indels 20; Gaps 5;
Db	404 NPDQVDPGVHCASTSNSNRNFEGRQGKGRTHLSPAMAAAAAINGHFEIDRK 454	Query Match	31.6%; Score 1282; DB 16; Length 456;
RN	[1]	RESULT 24	3
RP	Q99SJ3	SEQUENCE FROM N.A.	4
RC	ID Q99SJ3	PRELIMINARY;	5
RC	AC Q99SJ3; 2001 (TREMBLrel. 17, Created)	PRT;	6
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)	PRT;	7
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)	PRT;	8
DE	3-isopropylmalate dehydratase large subunit.	PRT;	9
GN	Staphylococcus aureus (strain Mu50 / ATCC 700699), and	PRT;	10
OS	Staphylococcus aureus (strain Mu50 / ATCC 700699), and	PRT;	11
GN	Staphylococcus aureus (strain N315), and	PRT;	12
OS	Staphylococcus aureus (strain Mu50 / ATCC 700699), and	PRT;	13
GN	Staphylococcus aureus (strain Mu50 / ATCC 700699), and	PRT;	14
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;	PRT;	15
OC	Bacillales; Firmicutes; Bacteria; Proteobacteria; gamma subdivision; Buchnera aphidicola.	PRT;	16
OX	Plasmid plieu.	PRT;	17
OC	Bacteria; Proteobacteria; gamma subdivision; Buchnera.	PRT;	18
OC	NCBi TaxID:9;	PRT;	19
RN	[1]	SEQUENCE FROM N.A.	20
RP	RE	PRELIMINARY;	21
RC	Q9EVH1	PRT;	22
RC	ID Q9EVH1	PRT;	23
AC	Q9EVH1; 2001 (TREMBLrel. 16, Created)	PRT;	24
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	PRT;	25
DT	01-MAR-2002 (TREMBLrel. 21, Last annotation update)	PRT;	26
DE	Isopropylmalate dehydratase subunit (Fragment).	PRT;	27
GN	Buchnera aphidicola.	PRT;	28
OS	Plasmid plieu.	PRT;	29
OC	Bacteria; Proteobacteria; gamma subdivision; Buchnera.	PRT;	30
OC	NCBi TaxID:9;	PRT;	31
RN	[1]	SEQUENCE FROM N.A.	32
RP	RE	PRELIMINARY;	33
RC	Q9EVH1	PRT;	34
AC	Q9EVH1; 2001 (TREMBLrel. 16, Created)	PRT;	35
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	PRT;	36
DT	01-MAR-2002 (TREMBLrel. 21, Last annotation update)	PRT;	37
DE	Isopropylmalate dehydratase subunit (Fragment).	PRT;	38
GN	Buchnera aphidicola.	PRT;	39
OS	Plasmid plieu.	PRT;	40
OC	Bacteria; Proteobacteria; gamma subdivision; Buchnera.	PRT;	41
OC	NCBi TaxID:9;	PRT;	42
RN	[1]	SEQUENCE FROM N.A.	43
RP	RE	PRELIMINARY;	44
RC	Q9EVH1	PRT;	45
AC	Q9EVH1; 2001 (TREMBLrel. 16, Created)	PRT;	46
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	PRT;	47
DT	01-MAR-2002 (TREMBLrel. 21, Last annotation update)	PRT;	48
DE	Isopropylmalate dehydratase subunit (Fragment).	PRT;	49
GN	Buchnera aphidicola.	PRT;	50
OS	Plasmid plieu.	PRT;	51
OC	Bacteria; Proteobacteria; gamma subdivision; Buchnera.	PRT;	52
OC	NCBi TaxID:9;	PRT;	53
RN	[1]	SEQUENCE FROM N.A.	54
RP	RE	PRELIMINARY;	55
RC	Q9EVH1	PRT;	56
AC	Q9EVH1; 2001 (TREMBLrel. 16, Created)	PRT;	57
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	PRT;	58
DT	01-MAR-2002 (TREMBLrel. 21, Last annotation update)	PRT;	59
DE	Isopropylmalate dehydratase subunit (Fragment).	PRT;	60
GN	Buchnera aphidicola.	PRT;	61
OS	Plasmid plieu.	PRT;	62
OC	Bacteria; Proteobacteria; gamma subdivision; Buchnera.	PRT;	63
OC	NCBi TaxID:9;	PRT;	64
RN	[1]	SEQUENCE FROM N.A.	65
RP	RE	PRELIMINARY;	66
RC	Q9EVH1	PRT;	67
AC	Q9EVH1; 2001 (TREMBLrel. 16, Created)	PRT;	68
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	PRT;	69
DT	01-MAR-2002 (TREMBLrel. 21, Last annotation update)	PRT;	70
DE	Isopropylmalate dehydratase subunit (Fragment).	PRT;	71
GN	Buchnera aphidicola.	PRT;	72
OS	Plasmid plieu.	PRT;	73
OC	Bacteria; Proteobacteria; gamma subdivision; Buchnera.	PRT;	74
OC	NCBi TaxID:9;	PRT;	75
RN	[1]	SEQUENCE FROM N.A.	76
RP	RE	PRELIMINARY;	77
RC	Q9EVH1	PRT;	78
AC	Q9EVH1; 2001 (TREMBLrel. 16, Created)	PRT;	79
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	PRT;	80
DT	01-MAR-2002 (TREMBLrel. 21, Last annotation update)	PRT;	81
DE	Isopropylmalate dehydratase subunit (Fragment).	PRT;	82
GN	Buchnera aphidicola.	PRT;	83
OS	Plasmid plieu.	PRT;	84
OC	Bacteria; Proteobacteria; gamma subdivision; Buchnera.	PRT;	85
OC	NCBi TaxID:9;	PRT;	86
RN	[1]	SEQUENCE FROM N.A.	87
RP	RE	PRELIMINARY;	88
RC	Q9EVH1	PRT;	89
AC	Q9EVH1; 2001 (TREMBLrel. 16, Created)	PRT;	90
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	PRT;	91
DT	01-MAR-2002 (TREMBLrel. 21, Last annotation update)	PRT;	92
DE	Isopropylmalate dehydratase subunit (Fragment).	PRT;	93
GN	Buchnera aphidicola.	PRT;	94
OS	Plasmid plieu.	PRT;	95
OC	Bacteria; Proteobacteria; gamma subdivision; Buchnera.	PRT;	96
OC	NCBi TaxID:9;	PRT;	97
RN	[1]	SEQUENCE FROM N.A.	98
RP	RE	PRELIMINARY;	99
RC	Q9EVH1	PRT;	100
AC	Q9EVH1; 2001 (TREMBLrel. 16, Created)	PRT;	101
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	PRT;	102
DT	01-MAR-2002 (TREMBLrel. 21, Last annotation update)	PRT;	103
DE	Isopropylmalate dehydratase subunit (Fragment).	PRT;	104
GN	Buchnera aphidicola.	PRT;	105
OS	Plasmid plieu.	PRT;	106
OC	Bacteria; Proteobacteria; gamma subdivision; Buchnera.	PRT;	107
OC	NCBi TaxID:9;	PRT;	108
RN	[1]	SEQUENCE FROM N.A.	109
RP	RE	PRELIMINARY;	110
RC	Q9EVH1	PRT;	111
AC	Q9EVH1; 2001 (TREMBLrel. 16, Created)	PRT;	112
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	PRT;	113
DT	01-MAR-2002 (TREMBLrel. 21, Last annotation update)	PRT;	114
DE	Isopropylmalate dehydratase subunit (Fragment).	PRT;	115
GN	Buchnera aphidicola.	PRT;	116
OS	Plasmid plieu.	PRT;	117
OC	Bacteria; Proteobacteria; gamma subdivision; Buchnera.	PRT;	118
OC	NCBi TaxID:9;	PRT;	119
RN	[1]	SEQUENCE FROM N.A.	120
RP	RE	PRELIMINARY;	121
RC	Q9EVH1	PRT;	122
AC	Q9EVH1; 2001 (TREMBLrel. 16, Created)	PRT;	123
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	PRT;	124
DT	01-MAR-2002 (TREMBLrel. 21, Last annotation update)	PRT;	125
DE	Isopropylmalate dehydratase subunit (Fragment).	PRT;	126
GN	Buchnera aphidicola.	PRT;	127
OS	Plasmid plieu.	PRT;	128
OC	Bacteria; Proteobacteria; gamma subdivision; Buchnera.	PRT;	129
OC	NCBi TaxID:9;	PRT;	130
RN	[1]	SEQUENCE FROM N.A.	131
RP	RE	PRELIMINARY;	132
RC	Q9EVH1	PRT;	133
AC	Q9EVH1; 2001 (TREMBLrel. 16, Created)	PRT;	134
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	PRT;	135
DT	01-MAR-2002 (TREMBLrel. 21, Last annotation update)	PRT;	136
DE	Isopropylmalate dehydratase subunit (Fragment).	PRT;	137
GN	Buchnera aphidicola.	PRT;	138
OS	Plasmid plieu.	PRT;	139
OC	Bacteria; Proteobacteria; gamma subdivision; Buchnera.	PRT;	140
OC	NCBi TaxID:9;	PRT;	141
RN	[1]	SEQUENCE FROM N.A.	142
RP	RE	PRELIMINARY;	143
RC	Q9EVH1	PRT;	144
AC	Q9EVH1; 2001 (TREMBLrel. 16, Created)	PRT;	145
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	PRT;	146
DT	01-MAR-2002 (TREMBLrel. 21, Last annotation update)	PRT;	147
DE	Isopropylmalate dehydratase subunit (Fragment).	PRT;	148
GN	Buchnera aphidicola.	PRT;	149
OS	Plasmid plieu.	PRT;	150
OC	Bacteria; Proteobacteria; gamma subdivision; Buchnera.	PRT;	151
OC	NCBi TaxID:9;	PRT;	152
RN	[1]	SEQUENCE FROM N.A.	153
RP	RE	PRELIMINARY;	154
RC	Q9EVH1	PRT;	155
AC	Q9EVH1; 2001 (TREMBLrel. 16, Created)	PRT;	156
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	PRT;	157
DT	01-MAR-2002 (TREMBLrel. 21, Last annotation update)	PRT;	158
DE	Isopropylmalate dehydratase subunit (Fragment).	PRT;	159
GN	Buchnera aphidicola.	PRT;	160
OS	Plasmid plieu.	PRT;	161
OC	Bacteria; Proteobacteria; gamma subdivision; Buchnera.	PRT;	162
OC	NCBi TaxID:9;	PRT;	163
RN	[1]	SEQUENCE FROM N.A.	164
RP	RE	PRELIMINARY;	165
RC	Q9EVH1	PRT;	166
AC	Q9EVH1; 2001 (TREMBLrel. 16, Created)	PRT;	167
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	PRT;	168
DT	01-MAR-2002 (TREMBLrel. 21, Last annotation update)	PRT;	169
DE	Isopropylmalate dehydratase subunit (Fragment).	PRT;	170
GN	Buchnera aphidicola.	PRT;	171
OS	Plasmid plieu.	PRT;	172
OC	Bacteria; Proteobacteria; gamma subdivision; Buchnera.	PRT;	173
OC	NCBi TaxID:9;	PRT;	174
RN	[1]	SEQUENCE FROM N.A.	175
RP	RE	PRELIMINARY;	176
RC	Q9EVH1	PRT;	177
AC	Q9EVH1; 2001 (TREMBLrel. 16, Created)	PRT;	178
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	PRT;	179
DT	01-MAR-2002 (TREMBLrel. 21, Last annotation update)	PRT;	180
DE	Isopropylmalate dehydratase subunit (Fragment).	PRT;	181
GN	Buchnera aphidicola.	PRT;	182
OS	Plasmid plieu.	PRT;	183
OC	Bacteria; Proteobacteria; gamma subdivision; Buchnera.	PRT;	184
OC	NCBi TaxID:9;	PRT;	185
RN	[1]	SEQUENCE FROM N.A.	186
RP	RE	PRELIMINARY;	187
RC	Q9EVH1	PRT;	188
AC	Q9EVH1; 2001 (TREMBLrel. 16, Created)	PRT;	189
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	PRT;	190
DT	01-MAR-2002 (TREMBLrel. 21, Last annotation update)	PRT;	191
DE	Isopropylmalate dehydratase subunit (Fragment).	PRT;	192
GN	Buchnera aphidicola.	PRT;	193
OS	Plasmid plieu.	PRT;	194
OC	Bacteria; Proteobacteria; gamma subdivision; Buchnera.	PRT;	195
OC	NCBi TaxID:9;	PRT;	196
RN	[1]	SEQUENCE FROM N.A.	197
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RC	Q9EVH1	PRT;	199
AC	Q9EVH1; 2001 (TREMBLrel. 16, Created)	PRT;	200
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	PRT;	201
DT	01-MAR-2002 (TREMBLrel. 21, Last annotation update)	PRT;	202
DE	Isopropylmalate dehydratase subunit (Fragment).	PRT;	203
GN	Buchnera aphidicola.	PRT;	204
OS	Plasmid plieu.	PRT;	205
OC	Bacteria; Proteobacteria; gamma subdivision; Buchnera.	PRT;	206
OC	NCBi TaxID:9;	PRT;	207
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DE	Isopropylmalate dehydratase subunit (Fragment).	PRT;	214
GN	Buchnera aphidicola.	PRT;	215
OS	Plasmid plieu.	PRT;	216
OC	Bacteria; Proteobacteria; gamma subdivision; Buchnera.	PRT;	217
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RN	[1]	SEQUENCE FROM N.A.	219
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AC	Q9EVH1; 2001 (TREMBLrel. 16, Created)	PRT;	222
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	PRT;	223
DT	01-MAR-2002 (TREMBLrel. 21, Last annotation update)	PRT;	224
DE	Isopropylmalate dehydratase subunit (Fragment).	PRT;	225
GN	Buchnera aphidicola.	PRT;	226
OS	Plasmid plieu.	PRT;	227
OC	Bacteria; Proteobacteria; gamma subdivision; Buchnera.	PRT;	228
OC	NCBi TaxID:9;	PRT;	229
RN	[1]	SEQUENCE FROM N.A.	230
RP	RE	PRELIMINARY;	231
RC	Q9EVH1	PRT;	232
AC	Q9EVH1; 2001 (TREMBLrel. 16, Created)	PRT;	233
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	PRT;	234
DT	01-MAR-2002 (TREMBLrel. 21, Last annotation update)	PRT;	235
DE	Isopropylmalate dehydratase subunit (Fragment).	PRT;	236
GN	Buchnera aphidicola.	PRT;	237
OS	Plasmid plieu.	PRT;	238
OC	Bacteria; Proteobacteria; gamma subdivision; Buchnera.	PRT;	239
OC	NCBi TaxID:9;	PRT;	240
RN	[1]	SEQUENCE FROM N.A.	241
RP	RE	PRELIMINARY;	242
RC	Q9EVH1	PRT;	243
AC	Q9EVH1; 2001 (TREMBLrel. 16, Created)	PRT;	244
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	PRT;	245
DT	01-MAR-2002 (TREMBLrel. 21, Last annotation update)	PRT;	246
DE	Isopropylmalate dehydratase subunit (Fragment).	PRT;	247
GN	Buchnera aphidicola.	PRT;	248
OS	Plasmid plieu.	PRT;	249
OC			

RL	J. Bacteriol.	183:785-790 (2001).
DR	EMBL; AF197453; ARS3139; 1; -.	
DR	InterPro; IPR01030; Aconitase_N.	
DR	InterPro; IPR00430; LeuC.	
PFam	PF00330; aconitase; 1.	
PRINTS	PR00415; ACONITASE.	
DR	PRODOM; PD000511; Aconitase N.	
DR	TIGRFAM; TIGR00170; leuC; 1.	
DR	PROSITE; PS00050; ACONITASE_1; 1.	
DR	PROSITE; PS01244; ACONITASE_2; 1.	
KW	Plasmid.	
FT	NON_TER 442 AA; 442 MW; 7ACBB7267AC18982 CRC64; SEQUENCE	
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Best Local Similarity	56.0%; Pred. No. 3e-78;	Best Local Similarity
Matches	252; Conservative 74; Mismatches 113; Indels 11; Gaps 3	Matches
Db	3 KTYLYQKLYDHSVYNDQEKTSILYIDLHLHLHETVTSQAFESLNRKAKVRQPNKUTPATMD 62	KTYLYQKLYDHSVYNDQEKTSILYIDLHLHLHETVTSQAFESLNRKAKVRQPNKUTPATMD
QY	69 HNVPTTSRKALKDI-ASFKEEDSRTOCVTBEVNEKFVGTVFGLSDRQGTVHVTGPEQ 127	69 HNVPTTSRKALKDI-ASFKEEDSRTOCVTBEVNEKFVGTVFGLSDRQGTVHVTGPEQ
Db	63 HNVSTQI---KDINASGLM---AKQMEQLTNCNCFBNISLYDINPHQGVHVIAPES 115	HNVSTQI---KDINASGLM---AKQMEQLTNCNCFBNISLYDINPHQGVHVIAPES
QY	128 GFTLPGTIVVCGDSHTSTHAGCALAFGIGSEVERVHATOCILITKSKSKNRIQVDELA 187	128 GFTLPGTIVVCGDSHTSTHAGCALAFGIGSEVERVHATOCILITKSKSKNRIQVDELA
Db	116 GFTLPGTIVVCGDSHTSTHAGCALAFGIGSEVERVHATOCILITKSKSKNRIQVDELA 175	GFTLPGTIVVCGDSHTSTHAGCALAFGIGSEVERVHATOCILITKSKSKNRIQVDELA
QY	188 PGVSSKDVVTHAIGIIGTAGGTGAVIETFGSVIRSLNBEARMSICNMSIEGARAGRMWAP 247	188 PGVSSKDVVTHAIGIIGTAGGTGAVIETFGSVIRSLNBEARMSICNMSIEGARAGRMWAP
Db	176 KFTVAKODILFPIKLGKSSGCVVPEKCKLIIKKMSNEERTMTCNNMIAEMGAKSLIEP 235	KFTVAKODILFPIKLGKSSGCVVPEKCKLIIKKMSNEERTMTCNNMIAEMGAKSLIEP
QY	248 DEFTYAVKJNKVSPR-GLFWEOSLNWDTLSDKDYDFKFTTDSNLAPQITWTT 307	248 DEFTYAVKJNKVSPR-GLFWEOSLNWDTLSDKDYDFKFTTDSNLAPQITWTT
Db	236 DEFTYAVKJNKVSPR-GLFWEOSLNWDTLSDKDYDFKFTTDSNLAPQITWTT 293	DEFTYAVKJNKVSPR-GLFWEOSLNWDTLSDKDYDFKFTTDSNLAPQITWTT
QY	308 PEDVPIGCVPPDPEFATEAKKADGRMLQYMGKIAKJGPMEDIPDVQVFIGCTNSIE 367	PEDVPIGCVPPDPEFATEAKKADGRMLQYMGKIAKJGPMEDIPDVQVFIGCTNSIE
Db	294 PDDVVISDEKIPNTEFNCILVKKNAKAKSACEYVMGLKPTDYLTDIAIDKVFIGCTNARIE 353	PDDVVISDEKIPNTEFNCILVKKNAKAKSACEYVMGLKPTDYLTDIAIDKVFIGCTNARIE
QY	368 DLRAAAAVVKGKKGAPNPKSAMVPGSIVKTOEEGKDFEEAGFWREAGCSMILG 427	DLRAAAAVVKGKKGAPNPKSAMVPGSIVKTOEEGKDFEEAGFWREAGCSMILG
Db	354 DLRSASILKNNKQSVNNK-AIVVPGSLVKTQABEGLDKIFIDSGFWRLPGCSMILG 412	DLRSASILKNNKQSVNNK-AIVVPGSLVKTQABEGLDKIFIDSGFWRLPGCSMILG
QY	428 MNPDPLAOPERCASTSNRNFEGRQAGGRT 457	MNPDPLAOPERCASTSNRNFEGRQAGGRT
Db	413 MNRDLISLFGERCASASNRNFEGRQGRGRT 442	MNRDLISLFGERCASASNRNFEGRQGRGRT

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